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(54) Title: MODIFIED SEED STORAGE PROTEINS

(57) Abstract

The invention provides modified plant storage proteins, in which the modification is effected in the primary structure of the protein, and the tertiary and quaternary structure of the protein is retained. The site for modification is selected by reference to the three-dimensional structure of the protein, which has been newly established by the inventors. Modified DNA molecules, vectors, transgenic plants, and parts and products thereof are also claimed.

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MODIFIED SEED STORAGE PROTEINS

This invention relates to plant seed storage proteins, and in particular to methods of modifying said proteins at specific sites.

Background of the Invention

Over the last few years there has been dramatic progress in the development of gene transfer systems for higher plants, and systems are now available for monocotyledonous plants, as well as for a variety of dicotyledonous plants. It is now possible not only to introduce foreign genes (including non-plant genes) into plant cells and tissues, and to regenerate whole plants, but also to

control the site in the plant where such genes will be expressed. Methods for introducing genes into plants, and the prospects which these methods offer for applying genetic engineering methods to improvement of crops, have recently been reviewed (C.S. Gasser and R.T. Fraley (1989) Science 244 1293-1299); this review reflects the state of the art. International Patent Application No. WO/8903887 discloses a process for production of a mammalian peptide via expression of a modified seed storage protein gene in a transgenic plant. The most commonly used vector is *Agrobacterium tumefaciens* Ti plasmid, which is successful in transferring genetic information into a variety of dicotyledonous plants, including peas and beans. More recently, the plant virus geminivirus has been proposed as a general purpose vector for use with plants (Australian Patent Application No. 599609 (64380/86) by Monsanto Company and David Bisaro)

Genetic engineering of improved grain crops has been hampered by the lack of detailed structural information about functional storage proteins, which form the major protein component of plant seeds[1]. After synthesis and processing, these proteins are transported to membranous organelles, known as protein bodies, where they accumulate in large amounts[2-4]. Upon germination, they are degraded by endogenous proteases to provide nutrition for the growing plant[5]. Because of the high level of expression and subsequent accumulation of these proteins, they determine the nutritional value of the seed and dictate the requirement for supplements when the seed is used as foodstuff for man or domestic animals.

Most of the protein found in mature seeds belongs to a class called the seed storage proteins. This term is used to describe those proteins whose function is to provide, upon germination, a source of fixed carbon and nitrogen to sustain the early heterotrophic growth of the seedling. However, it is because of the importance of seeds to human nourishment that so much work has been directed at understanding seed proteins. Among the best characterised of the seed proteins

are those from the agriculturally important legumes, soya bean (*Glycine max*), garden pea (*Pisum sativum*) and French bean (*Phaseolus vulgaris*), although increasing attention is being given to food crops of the Third World, including cow pea (*Vigna unguiculata*), mung bean (*V. radiata*) and pigeon pea (*Cajanus cajan*).

As a whole, legume storage proteins, which are mostly of the salt-soluble globulin class, are a nutritionally-poor source of tryptophan and the sulphur-containing amino acids, methionine and cysteine, although some of the other protein fractions within the seed (for example the albumins) may have adequate levels of these essential amino acids. Much effort has been directed to improving the understanding of storage proteins so as to be able to manipulate their genes using methods such as recombinant DNA techniques, tissue culture and plant breeding in such a way as to enhance the nutritional value of seed proteins for human and other monogastric animals.

There are two major types of storage proteins in legume seeds, known respectively as vicilins and legumins, which are distinguishable by their sedimentation coefficients (7S/11S), oligomeric organisation (trimeric/hexameric) and polypeptide chain structure (single chain/disulphide linked pair of chains)[6-12]. Both types are found within an individual storage body[13,14]. Analysis of amino-acid sequence data from these two classes suggests that they may be evolutionarily and structurally related[15,16]. Clear sequence relationships have been established within the classes[12]. Furthermore, a sequence motif common to legumins and vicilins[15] has been found to occur twice in vicilins[16], suggesting a repeated structural motif in vicilins.

Genes encoding two vicilin-type proteins have been isolated from pea (*Pisum sativum*), and transgenically expressed in tobacco, and their regulatory DNA sequence elements have been identified; these sequences respectively

govern the specificity of expression and level of transcription (Newbigin, E.J. and T.J.V. Higgins: Proc. 8th Australian Biotechnology Conference, Sydney 1989, 104-109)

Attempts have been made to improve the functional properties and nutritional value of glycinin, one of the major storage proteins of soybean, by producing cDNAs encoding glycinins modified by deletion of subsequences and by addition of sequences encoding four continuous methionines. The authors have shown expression and accumulation of some of the mutant proteins in E. coli cells (Kim et al., 1990).

However, their result is inconclusive, at best preliminary, as no attempt is made at expression in plant systems. Furthermore, these authors were limited in that they could only make changes to highly variable regions of the sequence, and then only in an ad hoc fashion. Their methods cannot be generally applied across a spectrum of legumins or vicilins. Indeed, the regions they have modified are regions of low homology to the vicilins, and therefore of no immediate application to vicilins. Nevertheless, their work does underscore that it is realistic to make modified seed storage proteins with improved properties according to the present invention.

Another seed storage protein, arcelin, has been identified in certain wild forms of Phaseolus vulgaris (Romero A. et al (1986) Theor. Appl. Genet 72 123-128; Osborn et al. (1986) Theor. Appl. Genet. 71 847-855); these proteins are toxic to bruchid pests of beans, and transfer of the cloned arcelin gene to other bean plant confers insect resistance (European Patent Application No. 337750: The Plant Cell Research Institute Inc).

In order to enable us to engineer novel properties into seeds without prejudicing their performance in vivo, we have for the first time determined the three-dimensional structure of phaseolin, the major 7S storage protein from the French Bean Phaseolus vulgaris. With this structural information, we can select suitable sites for modification.

Specific protein engineering targets in this system include improved nutritional value, altered stability with respect to functionality in food systems, and general use as a high-level expression system.

Phaseolin, a vicilin-like molecule, is a trimer of three similar glycosylated polypeptides of molecular weights around 50 000[17]. Unlike other vicilins, the phaseolin trimer (M_r about 150 000) associates into a dodecamer[18] below pH 4.5.

Because of the sequence and structural relationships between vicilins and legumins referred to above and further discussed hereinafter, we consider that phaseolin is a suitable model for legume 7S and 11S storage proteins in particular, and seed storage 7S and 11S proteins in general. Phaseolin has been expressed in transgenic plants[45].

Madison et al. have recently used the three-dimensional structure of the complex between trypsin and bovine pancreatic tissue inhibitor to predict the site of interaction between tissue plasminogen activator (tPA) and plasminogen activator inhibitor-1 (PAI-1). Although the three-dimensional structures of tPA and PAI-1 are not known, tPA and trypsin have sequence similarities. Using these similarities, the authors identified a loop, and one particular residue within the loop, which forms part of the interactive surface between PAI-1 and tPA; by changing the sequence of this loop by site-directed mutagenesis, they produced tPA which was less susceptible to inhibition (E.L. Madison, E.J. Goldsmith, R.D. Gerard, M-J.H. Gething, and J.F. Sambrook (1989) Nature <u>339</u> 721-724).

This strongly suggests that the three-dimensional structure of phaseolin can be used to predict the three-dimensional structures of other vicilins and of legumins.

We have found that the polypeptides of the trimeric seed storage protein phaseolin comprise two structurally-similar units each made up of a β-barrel and an α-helical domain. The β-barrel has the "jelly-roll" folding

topology shown by viral coat proteins and the α-helical domain shows structural similarity to the helix-turn-helix motif found in certain DNA-binding proteins. The tetramer of trimers referred to above turns out to be the form of the molecule in the crystals studied here.

Current experience suggests that protein structure is remarkably stable to manipulation by site-directed mutagenesis. Moreover, functional properties of α/β barrel proteins, 8-stranded β-barrel enzymes, and four-helix frameworks are stable to insertions and other modifications (reviewed by D. Ringe (1989) Nature 339 658-9).

Summary of the Invention

The major barrier to modifying plants to produce seed storage proteins with commercially desirable properties is knowledge of the three-dimensional structure of the storage proteins.

We have now determined the three-dimensional structure of a representative seed storage protein, phaseolin. Current knowledge in the construction of transgenic plants, and in protein structure and engineering, enables us to use this three-dimensional structure to select target sites in the structure for one or more of the following modifications:

(a) introduction of point mutations;
(b) deleting or inserting sequences;
(c) adding glycosylation sites;
(d) introducing disulphide bonds.

Thus, based on the three-dimensional structure disclosed herein, and experimental protocols known to persons skilled in the art, the following modifications can be made:

(i) Introduction of new N-linked glycosylation sites for altering the stability and/or solubility of the protein;
(ii) Substitution of internal amino acids by methionine to raise the sulphur content of the seed;

(iii) Truncation of protease-susceptible loops on the structure to improve stability;

(iv) Introduction of protease-labile loops to improve the digestive properties;

(v) Introduction of disulphide bonds or other stabilising mutations to protect the storage protein structure on passage through the rumen to improve the nutritional value of the protein for ruminants;

(vi) Introduction of heterologous protein or peptide sequences into the structure to enable their production in crops; and

(vii) Modifications to the sequence to enhance resistance of the seeds or products thereof to pests such as insects.

Aspects of these properties that are relevant in food systems include:

(a) stability and pH solubility for the large scale extraction of the proteins from seeds;

(b) acid solubility for protein enriched beverages;

(c) thermostability for heat-setting properties in snack foods; and

(d) amino acid composition for nutritional balance.

In one aspect, the present invention provides a mutein which is a variant of a naturally-occurring legume seed storage protein, wherein said mutein has a modified primary structure relative to said legume storage protein, but retains the tertiary and quaternary structure of said legume storage protein.

For the purposes of this specification, retention of the tertiary and quaternary structure is to be understood to mean that elements of that tertiary and quaternary structure which are not the subject of primary structure modifications are substantially unaffected by said modifications.

Thus according to one preferred embodiment of the present invention there is provided a plant 7S or 11S storage protein modified at a specific amino acid residue or a specific region of its amino acid sequence, wherein the tertiary and quarternary structure of the naturally occurring storage protein is retained.

Preferably the modification is selected from the group consisting of:

(a) introduction of one or more point mutations;

(b) deletion of one or more defined sequences of amino acids;

(c) insertion of one or more defined sequences of amino acids;

(d) introduction of one or more glycosylation sites; and

(e) introduction of one or more disulphide bonds.

More preferably the modification is selected from the group consisting of:

(a) introduction of N-linked glycosylation sites;

(b) substitution of internal amino acids by methionine;

(c) truncation of protease-labile loops; and

(d) introduction of protease-labile loops.

According to a second aspect of the invention, there is provided a DNA molecule whose sequence encodes a mutein, as defined above. Preferably this DNA encodes a protein having the properties of a plant 7S or 11S storage protein, and also encodes one or more of the modifications set out above. Plasmids, expression vectors, and microorganisms comprising said DNA are also within the scope of the invention.

According to a third aspect of the invention there is provided a transgenic plant or part thereof having a DNA sequence as defined above.

Preferably the plant part is a seed.

It will be evident to the person skilled in the art that the changes to the seed storage proteins provided by the method according to the invention will have to be made in the first instance at the DNA level. The modified DNA thus represents the initial embodiment of the changes; such DNA will be converted, via the processes of transcription and translation in the cell, to yield the modified seed storage protein.

Brief Description of the Drawings

Figure 1 (25 sheets) represents the atomic co-ordinates of phaseolin in orthogonal Å units. The three-fold symmetry axis of the phaseolin trimer is coincident with the Y axis of the co-ordinate frame. The coordinates of the C atoms have been deposited by the applicant in the Brookhaven Protein Data Bank.

Figure 2 represents schematic diagrams showing the two observed patterns of interaction between the $\alpha+\beta$ structural units. The absence of residues 213-219 in the electron density map leaves an ambiguity as to which is the correct pairing of the $\alpha+\beta$ units to form the polypeptide. (a) represents the preferred polypeptide (see text). In both diagrams the view is down the molecular three-fold axis and from the centre of the tetramer outwards. The pseudo-diads relating the structural units lie in the plane of the paper, intersecting the molecular three-fold.

Figure 3 represents a stereo pair showing a Cα trace of the phaseolin trimer, viewed down the molecular three-fold towards the centre of the tetramer. The N- and C-termini of each subunit are labelled. The two possible ways of linking the two $\alpha+\beta$ units to form the subunit are indicated: the shorter link of 17Å (solid line) is favoured above the longer 34Å link (dashed line). The figure was drawn using a computer program written by Lesk and Hardman[31].

Figure 4 is a diagram showing the structure of native phaseolin (A) and the proposed high-methionine mutant phaseolin (B) in the neighbourhood of residues 84 to 88. The methionine sidechains of the mutant are seen to be accommodated in the structure without disruption to the tertiary or quaternary structure of the protein. For clarity, residues in the same β-sheet as residues 84 to 88 are not shown.

Figure 5 is a diagram showing the structure of native phaseolin (A) and the proposed high-methionine mutant phaseolin (B) in the neighbourhood of residues 261-265. The methionine sidechains of the mutant are seen to be accommodated in the structure without disruption to the tertiary and quaternary structure of the protein. For clarity, residues in the same β-sheet as residues 261-265 are not shown.

Structure Description

X-ray diffraction data to 3Å resolution were collected from Type II crystals of phaseolin[19] and heavy atom derivatives. The methods of analysis do not form part of this invention. However, various attempts to solve the structure by multiple isomorphous replacement and non-crystallographic symmetry averaging were unsuccessful over a period of 6 years, until a cautious approach using phase extension procedures was adopted.

Structural heterogeneity

Three different genes encoding potential protein products have been identified by gene sequencing[11]. These differ only in number of amino acids, and contain 397, 411 and 412 amino acids respectively, after allowing for cleavage of a 24 amino-acid signal sequence. The sequence and numbering used here is given in Table 1.

```
                                  A'     A                   B
  1 TSLREEEESQDNPFYFNSDNSWNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSK 60
    [     V  ]............βββββ..ββββββ..............ββββββββ.

        C       D        E         F          G      H
 61 PETLLLPQQADAELLLVVRSGSAILVLVKPDDRREYFFLTSDNPIFSDHQKIPAGTIFYL 120
    ...βββββββ.ββββββββ.I.ββββββ.....ββββββββ......Vβββ....βββββ

            I        J         1      2       3
121 VNRDPKEDLRIIQLAMPVNNPQIHEFFLSSTEAQQSYLQEFSKHILEASFNSKFEEINRV 180
    β.......ββββββββ.......βIββ........ααααα.αααααααααI.αααααααα

                     4                  A'     A
181 LFEEEGQQEGVIVNIDSEQIKELSKHAKSSSRKSLSKQDNTIGNEFGNLTERTDNSLNVL 240
    α......V........αααααααααααααααα[      V]ββββ....Gβββββββ..βββ

      B      C       D       E              F     G
241 ISSIEMEEGALFVPHYYSKAIVILVVNEGEAHVELVGPKGNKETLEYESYRAELSKDDVF 300
    βββββββI..βββββββ...ββββββββ..βββββ......V......βββββ....βββ.

       H      I        J        1       2
301 VIPAAYPVAIKATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSG 360
    β.....βββββ...ββGββββββ.....βββββ.I....ααααααα..αααααααααα..

       3
361 SGDEVMKLINKQSGSYFVDAHHHQQEQQKGRKGAFVY
    .αααααααααα.........[                  ]
```

Table 1. Amino-acid sequence of the shorter (397 residue) β-type phaseolin polypeptide. The line underneath the sequence contains the following symbols. α: regions of α-helical secondary structure, β: regions of β-sheet secondary structure, G: glycosylation sites, [ ]: regions of unobserved electron density, I: intron locations, V: points of major sequence insertion in other vicilin proteins. Shown above the sequence are the labels used to denote the secondary-structural elements in the text. Note that the secondary structure assignments are based on the current unrefined model and thus that the precise start and end points of the strands and helices may be in error by one or two amino acids in some places.

Compared with the 397 residue protein,the 411 residue protein has a five amino-acid insertion after residue 189 and a nine amino-acid insertion after residue 390. The 412 residue protein has a further insertion of one amino acid after residue 100. The chain trace of the electron density map (not shown) is that of the 397 amino-acid protein (termed the β-type polypeptide[11]) and shows no break or weakening of electron density in the vicinity of residue 189. We thus conclude that the 397 amino-acid protein is overwhelmingly dominant in the crystal. It will be clear to the person skilled in the art that these three genes can be readily interconverted, using presently available techniques. This invention is to be understood to apply to all three forms of the protein.

The map shows weak evidence of glycan binding at both known Asn-X-Ser/Thr glycosylation triplets[24]. The density is not yet sufficiently clear to provide information about the nature of heterogeneity of the glycans.

Folding topology

Figure 2 shows a schematic drawing of the polypeptide. It consists of two structurally-similar units of about 160 amino acids each. These are related by a pseudo-diad axis nearly perpendicular to and intersecting the molecular triad axis. Each unit is itself an $\alpha + \beta$ two-domain structure, the first of some 110 residues being a classic viral capsid jelly-roll structure, and the second smaller domain being a cluster of three helices, including a helix-turn-helix motif. A fourth helix in the N-terminal unit, which is not structurally

associated with the three-helix cluster, forms part of the connection through to the C-terminal unit.

The jelly-roll barrel structure in phaseolin is stripped of nearly all of the elaboration seen in the viral capsid proteins[25,26]; in this respect it is similar to the barrel structure observed in catabolite gene activator protein (CAP)[27]. It is convenient to denote the eight strands of the jelly-roll β-barrel as B through I, in analogy with the notation used in the discussion of the viral capsid proteins[25]. In only two places in phaseolin is there found a loop of structure external to the barrel, between strands F and G of the N-terminal barrel (residues *ca* 102-108) and between strands E and F of the C-terminal barrel (residues *ca* 277-286). Each barrel has an A strand reminiscent of the C subunits of the plant virus capsid proteins[25], and another β-strand, antiparallel and N-terminal to A, which we label here strand A'. Both barrels have a further strand (which we label J) C-terminal to the barrel, making a total of eleven strands in the β-sheet structure. Strands C of each barrel have a bulge at positions 65-68 and 252-255 respectively.

The helical domains comprise residues *ca* 156-181 and 340-371, each being a three-helix cluster. These helices bear a striking similarity to a helix-turn-helix motif in Cro, a DNA binding protein[28]. This will be discussed further below. The occurrence on a single polypeptide of a jelly-roll β-barrel and a helical cluster reminiscent of DNA binding proteins has previously been observed for the CAP protein. However, the

relative position of these two domains in phaseolin and CAP is very different.

The internal sequence repeat[16] observed in phaseolin, jack bean canavalin and pea vicilin is the basis for the structural repeat described here. The sequence similarity in the internal repeat is low (≈15% identity), but the amino-acid alignment corresponds to the structural repeat perfectly in many places and to within a few residues in the worst cases. The domains are remarkably similar; a least-squares fit of the Cα positions in corresponding structural elements of the pair of units yields an r.m.s. deviation of only 2.2Å.

Exon/intron boundaries are the same in phaseolin and conglycinin DNA sequences[29,7,12]. Those five boundaries are, in the first unit, at the DE corner (residue 81), within the J β-strand (144), the H2-H3 corner (171); and in the second unit, the BC corner (248) and the β->α connection (335). If strand J is considered as a linking element between the β and α structures, then all these boundaries lie at the interconnection of various elements of the secondary structure.

Trimer structure

The six structural α+β units which comprise the phaseolin trimer are arranged alternately up and down around the three-fold axis and are nearly coplanar. The trimer is therefore a disc of diameter 90Å and thickness 35Å, as predicted by electron microscopy[30] and exhibits approximate 32

point group symmetry. Such an arrangement suggests two types of 'interfaces' between the units, intrachain contacts within one polypeptide, and trimer contacts between the three chains. Each interface is centred around a pseudo-diad relating the two structurally-similar units of the polypeptide. No electron density is visible for the region linking the units (residues 213-219) leaving an apparent ambiguity as to which adjacent pair of units in the trimer is on the one polypeptide chain (see Figure 3). One pair has a distance of 37Å between the Cα positions of residues 212 and 220, and the other has a corresponding distance of 18Å. To avoid postulating an extremely extended polypeptide linker, we conclude tentatively that the subunit is most likely formed from the latter pair. (The question of definition of the trimer within the tetramer will be discussed below; for completeness it should be pointed out that it is not possible for the missing polypeptide link to run from an N-terminal unit in one trimer to the C-terminal unit in another as these are separated by ≈ 60Å).

The jelly-roll β-barrel has a remarkable capacity to exist in different states of oligomerization[32,33]. The hexameric pattern observed here with quasi-32 point group symmetry is unlike the packing around the quasi-6-fold axis of the T=3 icosahedral surface lattice[26]. Furthermore the specific interactions between the barrels seen here are unlike those observed in T=1 capsids[25], tumour necrosis factor[34] or in the adenovirus hexon[33].

The B-I-D-G face of the two barrels associate with each around

the pseudo-diad in what appears to be a typical example of aligned packing of β-sheets. The two potential N-linked glycosylation sites are both within the C-terminal barrel on strands A and I respectively. The sugar attached to strand I could contact the neighbouring N-terminal barrel.

The helical domains of the subunits are closely associated with each other around the pseudo-diad relating the neighbouring subunits (see Figure 2b). As mentioned above, the helix-turn-helix motifs formed by helices 2 and 3 of each domain are similar to those found in certain DNA-binding proteins[35], typified by the Cro protein. A least-squares fit of the Cα positions of residues 163-183 and 351-371 of phaseolin to the helix-turn-helix motif formed by residues 16-36 of Cro yields an r.m.s. deviation of 1.9Å and 1.3Å respectively, within the spread determined for these motifs[35]. The capacity of helix-turn-helix structures to bind DNA is associated with their condensation into dimers with diad symmetry coincident with that of double-stranded DNA, in particular with elements of the diad-related helices positioned 34Å apart and binding to consecutive major grooves of DNA. No such 34Å period is evident in the dimerisation of the phaseolin helical domains, nor indeed are the two domains identical. The dimensions of that domain pair are more of the order of 18Å (in the trimer, not the polypeptide as we have chosen to define it here, Figure 3), sufficient only to span adjacent major and minor grooves of DNA. All of the DNA-protein structures solved to date which have helix-turn-helix motifs for the DNA binding site exemplify the diad-symmetrical form of binding.

Recent studies[35,36] of structures in the protein data bank[37] have demonstrated that DNA binding protein II[38], the ribosomal L7/L12 protein[39] and cytochrome C peroxidase[40] all contain helix-turn-helix motifs. The first two of these bind nucleic acids, whether or not via the helix-turn-helix motif is unknown. However the cytochrome C peroxidase structure embodies the motif semi-internally, making interaction with DNA very unlikely[35].

In phaseolin the second helix in the motif (i.e. the third in the helical domain) is exposed to the environment in both structural units on the polypeptide and within the trimer (Figure 3). We know of no evidence suggesting that phaseolin is able to bind DNA, specifically or non-specifically. The translocation of the phaseolin polypeptide from its site of synthesis on membrane-bound polysomes through the endoplasmic reticulum into storage bodies[41,3] makes such an interaction unlikely. Nevertheless, DNA-binding studies could provide direct evidence for or against a role for storage proteins in the regulation of their own high level of synthesis.

Ligand binding sites

We have previously reported[19] the results of a phosphorus analysis of type II phaseolin crystals which implies that two molecules of phytic acid might be associated with each 50kDa polypeptide. There is no electron-dense feature in the current 3Å map consistent with such binding, though phytate binding to

the flexible ends or linker region of the polypeptide cannot be excluded.

At the interface between the two jelly-roll domains of the subunit involving the sheets B-I-D-G referred to above, there is an intense spherical electron-dense feature lying in a pocket formed by the side chains of residues His 32, Glu 56, Arg 58, Arg 79, Arg 130, Lys 296 and Asp 297. A possible explanation is that it corresponds to phosphate bound either *in vivo* or during the purification process. A second unexplained, though more diffuse, electron-dense feature occurs within the N-terminal β-barrel and is associated with the side chains of residues Gln 133 and Glu 145.

The tetramer of trimers

The crystallization conditions used here for phaseolin have encouraged the formation of tetrameric 18S particles. The association of trimers into dodecamers under conditions of acid pH is well-characterized[18], and 18S particles so produced have been imaged by electron microscopy[30]. The 18S particle observed in the crystal, being formed by four trimers assembled on the faces of a regular tetrahedron, is consistent with the negatively stained e.m. image as judged by the positioning of the solvent channels.

There are two ways of grouping the twelve subunit polypeptide chains in the tetrahedron into trimers. Inspection of the particle shows that in the one association, the intra-trimer

polypeptide contacts are extensive (see Figure 3) whereas in the alternate association the subunits are tenuously packed (reminiscent of protein crystal packing). We conclude that the former arrangement is the 7S (150kDa) particle occurring *in vivo* and observed as a featureless disc by electron microscopy[30], and have used this definition of the trimer in the discussion of the preceding sections. The inter-trimer contact in the tetramer occurs at the tetrahedral diad axes. It consists of a symmetry-related pair of interactions, each involving the N-terminal β-barrel of one subunit with the C-terminal β-barrel of a subunit from the neighbouring trimer. The N-terminal strands of polypeptides from neighbouring trimers are also in contact at the tetrahedral diad.

In situ organization

Although no crystallinity of *Phaseolus vulgaris* seed sections is observable by X-ray diffraction[19], we cannot rule out a possible link between the curious packing of phaseolin in pseudo-cubic high-salt crystals[19,42] with structures *in situ* in the seed-storage protein body. (Such a link has been demonstrated for the 11S protein cucurbitin[43]). The high-saltcrystals, with pseudo -cubic symmetry P432 and cell dimension a ≈ 66Å, can contain only one phaseolin trimer per unit cell. What combination of crystal twinning and/or disorder generates the pseudo-cubic point group is unclear. One possibility emerges from the dodecamer structure observed here. The centre-to-centre distance between the trimers in the tetrahedral 18S particle is ≈ 65Å. Packing errors, whereby

trimers are incorporated into the tetrahedral structures without proper cognizance of the top and bottom face of the trimer, could lead to non-closed forms of the tetramer (of trimers) and an average structure in which the 65Å period was associated with a cubic point group. Other explanations include the possibility that the pseudo 32 point group of the trimer is not maintained in high salt, but is distorted into a quasi-cubic structure.

Related Structures

Homology with other vicilins

Sequence alignments imply structural similarity of 7S proteins from common bean, jack bean, soybean and pea seeds[12,15,16]. Insertions and deletions in these alignments are, with minor modifications, compatible with the phaseolin structure (see Table 1). For the most part, the phaseolin sequence is shorter than the other sequences, the exception being a five residue insertion around position 350, which may affect the structure of the connection between helices 1 and 2 of the C-terminal structural unit. Significant insertions in the other sequences are found near the N-terminus and at the FG corner (residue 107, Table 1) of the first barrel domain (α'-subunit of β-conglycinin of soybean), in the linker between helices 3 and 4 (residue 188) of the first helical domain (pea vicilin), in the linker (residue 218) between the two α+β units (all sequences except phaseolin), and at the EF corner (residue 283) of the second barrel domain (larger inserts for pea proteins

than for soybean). All of these regions are on the surface of the trimer. (The insertion site at residue 218[15] has been placed alternatively at residue 247[12]; we consider that the former leads to the more natural sequence alignment).

A preliminary structure for jack bean canavalin (A.McPherson, personal communication) shows pseudo 32 point group symmetry and a viral capsid domain in each of the two structural units per polypeptide.

Homology with legumins

Based on amino-acid sequence similarity, the basic polypeptide chain of legumins is believed to contain one copy of the repeating structural unit of a vicilin molecule[16], i.e. the $\alpha+\beta$ structure described here. Weak similarity between parts of the acidic chain and the 7S proteins has also been reported, but is less convincing[15]. X-ray diffraction experiments[43] have indicated that the legumin protein cucurbitin has point group symmetry 23, at least at low resolution (*ca* 20Å). This observation requires that the polypeptide displays an internal repeating structure, which in the 11S particle is a diad, albeit not perpendicular to any three-fold axis. The assembly of the six polypeptides of legumin into the accumulated oligomeric form is believed to proceed via a 7S (trimer) intermediate, the final coalescing of trimers not occurring until cleavage of the polypeptides into the basic and acidic chains[44]. If the trimer form is indeed similar to the vicilin 7S molecules, with pseudo point group 32, then a rearrangement

of the subunits within the trimer must accompany the formation of the 11S particle, in order to satisfy the resulting cubic arrangement of diads and triads.

Novel phaseolins

One attempt has previously been made to increase the sulphur content of phaseolin by the insertion of a 45 base-pair synthetic duplex, rich in methionine-codons, at the Xba I site[7] in the third exon of the β-phaseolin gene. Transgenic tobacco plants containing normal or modified phaseolin genes were then monitored for the production and deposition of phaseolin. Whereas in both cases phaseolin expression was achieved, deposition of the modified protein in the storage bodies did not occur, suggesting prior degradation[45]. Using the three-dimensional structure, we are now able to identify the Xba I site (after residue 165, Table 1) as being internal to helix 2 (i.e. the first helix in the helix-turn-helix motif) and hence part of a major structural element of the phaseolin trimer. We therefore predict that an inclusion of fifteen residues at this site could distort the structure at the tertiary and/or quaternary level, making the modified protein more susceptible to degradation.

Conclusions

We have now confirmed the internal repeat observed in the sequence of phaseolin at a structural level; this repeat manifests itself as a pair of $\alpha+\beta$ units forming the 50kDa subunit. The high sequence similarity to other 7S storage proteins suggests a common structure; indeed a preliminary X-ray structure for canavalin, the 7S protein of the jack bean, indicates a hexameric arrangement of β-barrels as described here (A. McPherson, personal communication).

The structure presented here identifies surface regions of the molecule, which represent candidate sites for genetically-engineered insertions into the sequence.

The invention will now be illustrated by way of reference only to the following non-limiting examples. The references to amino acid sequence numbering are as in Table 1.

In these examples, site directed mutagenesis is used to introduce desired mutations at defined sites in known fragments of wild type phaseolin cDNA.

Mutations are introduced by known methods, such as those described by Kunkel (46), into restriction fragments which include the segment of DNA encoding the locus for the desired mutation. The resulting DNA is used to transfect a host, such as E.coli, and single stranded DNA prepared from plaques. The presence of the desired mutation is confirmed by complete sequencing of the same restriction fragment, for example using the method of Sanger et al. (47). The double stranded replicative form of DNAs of proven mutants is isolated, and the mutant restriction fragments isolated by agarose electrophoresis (48). These fragments are then used to replace the corresponding fragment of wild type DNA in an expression vector. All the recombinant methods used are as described by Sambrook et al. (48). Other suitable methods for these procedures would readily occur to the person skilled in the art.

Example 1 - Engineering of High Methionine Phaseolin Mutations

The two sequences selected as targets for engineering of high-methionine phaseolins are "ILVLV" in region E between amino acids 61 and 120, Table 1 and "IVILV" in region D between amino acids 241 and 300, Table 1, which both correspond to hydrophobic domains, ie. regions of internal β structure. Each of these sequences is mutated to code for methionine pockets (MMMMM) by iterated cycles of oligonucleotide site-directed mutagenesis. An intron-less β-phaseolin minigene is mutated; this minigene, designated βwt^{i-}, has recently been shown to direct efficient expression of phaseolin protein in transgenic tobacco seeds (Bustos et al., 1990; (49)). The advantages of using the minigene

instead of phaseolin genomic DNA fragments derive from the absence of intervening sequences. This facilitates the design of gene constructions and permutations of DNA fragments to combine different mutations. Due to the large number of individual nucleotides that need to be mutated over a span of 15 or 18 nucelotides, a strategy involving multiple rounds of mutagenesis is preferable to one that would attempt to produce all changes at once. This has the added advantage of generating intermediates with fewer than five new methionines, which may be useful when assessing the effects of individual amino acid changes on the structure and *in vivo* stability of the protein. The detailed mutagenesis strategies are as follows:

"ILVLV" site:

A 381 bp EcoRI-PstI restriction fragment from clone βwt^{i-}(Bustos et al., 1990) is subcloned into the phagemid vector pBSKS+ (Stratagene) and the resulting clone is used to produce a U-containing single stranded DNA template. Three different synthetic single-stranded oligonucleotide DNA molecules (shown below as oligos I to III) are utilized to mutagenize the wt sequence by the method of Kunkel (46). The individual base substitutions are indicated in boldface. Screening of mutated clones is performed directly by sequencing with an oligonucleotide primer designed to hybridize 35 nucleotides upstream of the target sequences.

		^{81}gly	ser	ala	Ile	Leu	Val	Leu	Val	lys	pro	asp^{91}	
wt	...	ggg	agc	gcc	ATA	CTC	GTC	TTG	GTG	aaa	cct	gat	...
oligo I			$^{5'}$agc	gcc	ATG	ATG	GTC	TTG$^{3'}$					
oligo II							$^{5'}$G GTC	TTG	ATG	aaa	cct$^{3'}$		
oligo III				$^{5'}$gcc	ATG	ATG	ATG	ATG	ATG	aaa	cct$^{3'}$		
final		^{81}gly	ser	ala	Met	Met	Met	Met	Met	lys	pro	asp^{91}	
	...	ggg	agc	gcc	ATG	ATG	ATG	ATG	ATG	aaa	cct	gat	...

After each round of mutagenesis has been completed, the new EcoRI-PstI DNA fragments are replaced into the βwt^{i-} gene to yield modified phseolin genes coding for two, three and five new methionine residues.

"IVILV" site"

A 2.0 kbp XbaI-BamHI restriction fragment from clone βwt^{i-} (Bustos et al., 1990) is subcloned into the phagemid vector pBSKS+ (Stratagene) and the resulting clone used to produce a U-containing single-stranded DNA template. In a manner analogous to that employed at the ILVLV site, three synthetic oligonucleotides (oligos IV to VI, shown below) are used to mutagenize the wt sequence using the same method. As for the other site, each oligo is designed to mutate two or three closely spaced nucleotides, and all oligos result in at least one new methionine codon.

```
            258ser lys ala Ile Val Ile Leu Val val asn glu gly269
wt          ...tct aag gcc ATT GTT ATA CTA GTG gtt aat gaa gga ..
oligo IV         5'aag gcc ATG ATG ATA CTA GT3'
oligo V                         5'TG ATA CTG ATG gtt aat3'
oligo VI                    5'TG ATG ATG ATG ATG gtt31
final       258ser lys ala Met Met Met Met Met val asn glu gly269
            ...tct aag gcc ATG ATG ATG ATG ATG gtt aat gaa gga ..
```

As for the ILVLV site, the sequences at and around the mutated sites are verified using a sequencing primer that hybridizes near the site. After mutagenesis the XbaI-BamHI fragments are replaced into βwt^{i-} or into the high-methionine mutants modified at the ILVLV site. A maximum of ten new methionine residues result from the combination of mutations at both sites.

All mutated phaseolin genes are subsequently subcloned into the binary vector pBIN19 and transferred into the genome of tobacco by A. tumefaciens-mediated transformation.

Example 2 - Model Building of High-Methionine Mutant Phaseolin

The structure of the high-methionine mutant phaseolin can be investigated by model-building as follows. An interactive molecular-graphics computer program (QUANTA, Polygen Corporation) was used to model the replacement of residues 84 to 88 and 261 to 265 by methionine. The energy-refinement computer-program XPLOR (Harvard University) was then used to refine the atomic coordinates of the mutant structure to ensure that favourable stereochemistry is achieved, keeping the remainder of the protein as close as possible to the native structure. The results of the modelling are shown in Figures 4 and 5; there are no significant difference in energy between the native and mutant structures (native: -11529 Kcal/mol, mutant: -11677 Kcal/mol) and no disruption to the tertiary or quaternary structure is predicted.

Example 3

The environment of the following residues in the phaseolin structure indicates that they can be altered to Methionine without prejudice to the three-dimensional structure of the protein:

Leu 65, Leu 76, Phe 252, Leu 264, Ile 177, Leu 181.

Example 4

Mutation of Isoleucine 105 to Asparagine introduces an N-linked glycosylation site at that position. Sugar attached at that site may be accommodated on the surface of the phaseolin trimer.

Example 5

Elimination of the loop of structure between beta strands E and F of the C-terminal structural unit may be accomplished by deleting residues numbered 278 to 287 and

replacing them with a linker of two glycine residues. This increases the stability of phaseolin to enzymes with trypsin-like specificity.

In general, the selection of sites for mutagenesis may be influenced by the accessibility of the target site to restriction endonucleases. The criteria for assessing whether the desired mutation has been achieved will depend on the nature of the mutation attempted, but include;

a) sequencing of the DNA in the construct;
b) analysis of the product protein for presence or absence of the desired property, eg. by amino acid analysis or susceptibility to enzymes;
c) retention of tertiary or quaternary structure;
d) cross-reaction with antibody directed against the native protein; and
e) successful expression *in vivo*.

For example, if the mutation is to substitute methionine for another amino acid, the presence of one or two met residues could be detected by cyanogen bromide cleavage; the presence of about 10 met residues could be readily assayed by amino acid analysis. Retention of three dimensional structure (tertiary or quaternary) can be assessed in advance by model building, and tested in the protein actually produced by success in expression *in vivo*, and by various physical analyses such as molecular weight, solubility, and circular dichroism spectral studies. Other suitable methods will be known to those skilled in the art.

Although the invention has been illustrated with reference to phaseolin, sequence homologies indicate that similar results may be expected with related proteins, such as the homologous protein from pea, and to some extent with legumins as implied by the homology described in reference 16.

References cited herein are identified in full on the following pages.

It will be clearly understood that the invention in its general aspects is not limited to the specific details referred to hereinabove.

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CLAIMS:

1. A mutein which is a variant of a naturally-occurring legume seed storage protein, wherein said mutein has a modified primary structure relative to said legume storage protein, but retains the tertiary and quaternary structure of said legume storage protein.

2. A plant 7S or 11S storage protein modified at a specific amino acid residue or a specific region of its amino acid sequence, wherein the tertiary and quarternary structure of the naturally occurring storage protein is retained.

3. A storage protein according to Claim 1 or Claim 2, wherein the modification is selected from the group consisting of:

(a) introduction of one or more point mutations;

(b) deletion of one or more defined sequences of amino acids;

(c) insertion of one or more defined sequences of amino acids;

(d) introduction of one or more glycosylation sites; and

(e) introduction of one or more disulphide bonds.

4. A plant storage protein according to Claim 3, wherein the modification is selected from the group consisting of:

(a) introduction of N-linked glycosylation sites;

(b) substitution of internal amino acids by methionine;

(c) truncation of protease-labile loops; and

(d) introduction of protease-labile loops.

5. A protein according to any one of Claims 1 to 5 which is a vicilin or a legumin.

6. A protein according to Claim 5 which is a phaseolin.

7. A DNA molecule whose sequence encodes a storage protein as defined in any one of Claims 1 to 6.

8. A DNA molecule according to Claim 7, whose sequence encodes a protein having the properties of a plant 7S or 11S storage protein, and also encodes one or more of the modifications set out above.

9. A DNA molecule according to Claim 8 wherein the protein is a vicilin or a legumin.

10. A DNA molecule according to Claim 9 wherein the protein is phaseolin.

11. An autonomous unit of DNA replication *in vivo* or *in vitro* selected from the group consisting of plasmids, cosmids, expression vectors, microorganisms, viruses and chromosomes, said autonomous unit comprising a DNA molecule according to any one of Claims 7 to 10.

12. A autonomous unit of DNA replication according to Claim 11 which is *Agrobacterium tumefaciens*.

13. A autonomous unit of DNA replication according to Claim 11 which is a plant virus.

14. A transgenic plant or part thereof comprising a DNA sequence as defined in any one of Claims 7 to 10.

15. A seed of a transgenic plant according to Claim 14.

16. A product obtained from a plant according to Claim 14.

FIG. 1.1.

ASP	CB	11	2.38	-16.30	22.82	:	ASP	CG	11	3.50	3.50	23.77
ASP	OD1	11	3.32	-16.13	24.98	:	ASP	OD2	11	4.54	4.54	23.28
ASP	C	11	3.49	-18.33	21.93	:	ASP	O	11	4.63	4.63	21.67
ASP	N	11	2.22	-16.70	20.49	:	ASP	CA	11	3.07	3.07	21.63
ASN	N	12	2.64	-19.23	22.45	:	ASN	CA	12	2.97	2.97	22.44
ASN	CB	12	2.52	-21.35	23.74	:	ASN	CG	12	2.75	2.75	23.84
ASN	OD1	12	2.74	-23.40	24.91	:	ASN	ND2	12	3.03	3.03	22.85
ASN	C	12	2.17	-21.25	21.29	:	ASN	O	12	1.03	1.03	21.53
PRO	N	13	2.61	-21.42	20.06	:	PRO	CD	13	3.98	3.98	19.67
PRO	CA	13	1.81	-21.88	18.93	:	PRO	CB	13	2.73	2.73	17.79
PRO	CG	13	4.04	-22.16	18.43	:	PRO	C	13	1.15	1.15	19.00
PRO	O	13	0.33	-23.52	18.17	:	PHE	N	14	1.52	1.52	19.91
PHE	CA	14	0.98	-25.45	19.99	:	PHE	CB	14	2.02	2.02	20.44
PHE	CG	14	3.38	-26.29	19.80	:	PHE	CD1	14	3.66	3.66	18.58
PHE	CD2	14	4.30	-25.52	20.43	:	PHE	CE1	14	4.86	4.86	18.03
PHE	CE2	14	5.50	-25.25	19.85	:	PHE	CZ	14	5.78	5.78	18.66
PHE	C	14	-0.16	-25.56	20.96	:	PHE	O	14	-0.80	-0.80	21.03
TYR	N	15	-0.48	-24.55	21.74	:	TYR	CA	15	-1.51	-1.51	22.74
TYR	CB	15	-1.04	-23.99	24.00	:	TYR	CG	15	-2.10	-2.10	25.04
TYR	CD1	15	-2.89	-24.76	25.48	:	TYR	CE1	15	-3.83	-3.83	26.45
TYR	CD2	15	-2.24	-22.53	25.56	:	TYR	CE2	15	-3.17	-3.17	26.52
TYR	CZ	15	-3.95	-23.34	26.94	:	TYR	OH	15	-4.88	-4.88	27.88
TYR	C	15	-2.78	-24.04	22.24	:	TYR	O	15	-2.79	-2.79	22.14
PHE	N	16	-3.79	-24.86	21.99	:	PHE	CA	16	-5.13	-5.13	21.61
PHE	CB	16	-5.79	-25.46	20.73	:	PHE	CG	16	-5.13	-5.13	19.40
PHE	CD1	16	-5.78	-24.67	18.42	:	PHE	CD2	16	-3.89	-3.89	19.22
PHE	CE1	16	-5.15	-24.53	17.23	:	PHE	CE2	16	-3.26	-3.26	18.04
PHE	CZ	16	-3.90	-25.08	17.06	:	PHE	C	16	-5.97	-5.97	22.86
PHE	O	16	-6.47	-25.11	23.52	:	ASN	N	17	-6.17	-6.17	23.16
ASN	CA	17	-6.76	-22.52	24.39	:	ASN	CB	17	-6.43	-6.43	24.56
ASN	CG	17	-6.74	-20.63	25.93	:	ASN	OD1	17	-6.11	-6.11	26.28
ASN	ND2	17	-7.57	-21.19	26.78	:	ASN	C	17	-8.22	-8.22	24.31
ASN	O	17	-8.80	-22.09	23.39	:	SER	N	18	-8.90	-8.90	25.22
SER	CA	18	-10.32	-23.45	25.06	:	SER	CB	18	-10.82	-10.82	26.02
SER	OG	18	-10.32	-23.95	27.25	:	SER	C	18	-11.09	-11.09	25.21
SER	O	18	-12.27	-22.16	24.86	:	ASP	N	19	-10.50	-10.50	25.59
ASP	CA	19	-11.38	-19.92	25.67	:	ASP	CB	19	-11.09	-11.09	26.89
ASP	CG	19	-9.66	-18.65	27.12	:	ASP	OD1	19	-8.90	-8.90	26.16
ASP	OD2	19	-9.28	-18.47	28.26	:	ASP	C	19	-11.36	-11.36	24.38
ASP	O	19	-12.23	-18.33	24.14	:	ASN	N	20	-10.48	-10.48	23.44
ASN	CA	20	-10.77	-18.92	22.13	:	ASN	CB	20	-9.90	-9.90	21.92
ASN	CG	20	-8.44	-18.06	21.99	:	ASN	OD1	20	-8.00	-8.00	21.36
ASN	ND2	20	-7.62	-17.36	22.76	:	ASN	C	20	-10.63	-10.63	21.00
ASN	O	20	-10.65	-19.54	19.85	:	SER	N	21	-10.60	-10.60	21.17
SER	CA	21	-10.32	-22.16	20.06	:	SER	CB	21	-9.12	-9.12	20.37
SER	OG	21	-7.95	-22.29	20.01	:	SER	C	21	-11.35	-11.35	19.50
SER	O	21	-11.02	-23.76	18.51	:	TRP	N	22	-12.56	-12.56	20.03
TRP	CA	22	-13.55	-24.18	19.55	:	TRP	CB	22	-14.17	-14.17	20.68
TRP	CG	22	-13.30	-26.06	21.32	:	TRP	CD2	22	-13.16	-13.16	20.91
TRP	CE2	22	-12.30	-27.84	21.83	:	TRP	CE3	22	-13.63	-13.63	19.92
TRP	CD1	22	-12.56	-25.81	22.43	:	TRP	NE1	22	-11.96	-11.96	22.72
TRP	CZ2	22	-11.88	-29.14	21.77	:	TRP	CZ3	22	-13.22	-13.22	19.84
TRP	CH2	22	-12.36	-29.96	20.77	:	TRP	C	22	-14.63	-14.63	18.97
TRP	O	22	-14.82	-22.27	19.54	:	ASN	N	23	-15.38	-15.38	17.93
ASN	CA	23	-16.48	-22.68	17.69	:	ASN	CB	23	-16.46	-16.46	16.42
ASN	CG	23	-15.17	-21.91	15.61	:	ASN	OD1	23	-14.97	-14.97	14.72
ASN	ND2	23	-14.30	-20.93	15.85	:	ASN	C	23	-17.62	-17.62	17.49
ASN	O	23	-17.43	-24.56	16.75	:	THR	N	24	-18.70	-18.70	18.22
THR	CA	24	-19.99	-23.99	18.24	:	THR	CB	24	-20.90	-20.90	19.21

FIG. 1.2

THR	OG1	24	-20.10	-23.13	20.36	THR	CG2	24	-22.09	-22.09	19.57
THR	C	24	-20.70	-23.98	16.92	THR	O	24	-20.96	-20.96	16.33
LEU	N	25	-21.03	-25.17	16.47	LEU	CA	25	-21.71	-21.71	15.20
LEU	CB	25	-21.18	-26.50	14.51	LEU	CG	25	-21.94	-21.94	13.40
LEU	CD1	25	-21.94	-26.04	12.34	LEU	CD2	25	-21.35	-21.35	12.92
LEU	C	25	-23.17	-25.31	15.56	LEU	O	25	-23.92	-23.92	14.92
PHE	N	26	-23.63	-26.15	16.52	PHE	CA	26	-25.01	-25.01	16.98
PHE	CB	26	-25.77	-27.36	16.40	PHE	CG	26	-27.18	-27.18	16.95
PHE	CD1	26	-28.28	-27.02	16.36	PHE	CD2	26	-27.36	-27.36	18.05
PHE	CE1	26	-29.52	-27.25	16.86	PHE	CE2	26	-28.60	-28.60	18.54
PHE	CZ	26	-29.68	-28.04	17.95	PHE	C	26	-25.03	-25.03	18.50
PHE	O	26	-24.14	-26.94	19.07	LYS	N	27	-25.99	-25.99	19.20
LYS	CA	27	-26.12	-25.93	20.63	LYS	CB	27	-25.32	-25.32	21.50
LYS	CG	27	-25.70	-23.49	21.39	LYS	CD	27	-25.10	-25.10	22.49
LYS	CE	27	-25.27	-21.28	22.17	LYS	NZ	27	-24.14	-24.14	22.69
LYS	C	27	-27.58	-25.63	20.88	LYS	O	27	-28.17	-28.17	20.29
ASN	N	28	-28.17	-26.44	21.72	ASN	CA	28	-29.55	-29.55	22.09
ASN	CB	28	-30.45	-26.99	21.10	ASN	CG	28	-30.72	-30.72	21.53
ASN	OD1	28	-31.67	-28.55	22.24	ASN	ND2	28	-29.96	-29.96	21.53
ASN	C	28	-29.62	-26.85	23.50	ASN	O	28	-28.60	-28.60	24.01
GLN	N	29	-30.79	-26.93	24.11	GLN	CA	29	-30.78	-30.78	25.49
GLN	CB	29	-32.08	-26.99	26.19	GLN	CG	29	-33.27	-33.27	25.80
GLN	CD	29	-33.91	-27.26	24.52	GLN	OE1	29	-34.74	-34.74	23.94
GLN	NE2	29	-33.66	-26.09	23.97	GLN	C	29	-30.48	-30.48	25.70
GLN	O	29	-30.37	-29.15	26.88	TYR	N	30	-30.35	-30.35	24.65
TYR	CA	30	-30.02	-31.00	24.88	TYR	CB	30	-30.90	-30.90	24.08
TYR	CG	30	-32.32	-31.88	24.59	TYR	CD1	30	-32.70	-32.70	25.66
TYR	CE1	30	-34.00	-32.56	26.10	TYR	CD2	30	-33.19	-33.19	23.93
TYR	CE2	30	-34.49	-30.97	24.36	TYR	CZ	30	-34.90	-34.90	25.44
TYR	OH	30	-36.23	-31.63	25.84	TYR	C	30	-28.61	-28.61	24.58
TYR	O	30	-28.22	-32.54	24.90	GLY	N	31	-27.83	-27.83	23.93
GLY	CA	31	-26.44	-30.89	23.69	GLY	C	31	-25.81	-25.81	22.75
GLY	O	31	-26.45	-28.92	22.34	HIS	N	32	-24.57	-24.57	22.35
HIS	CA	32	-23.96	-29.18	21.40	HIS	CB	32	-23.29	-23.29	22.10
HIS	CG	32	-22.26	-28.49	23.13	HIS	CD2	32	-22.47	-22.47	24.46
HIS	ND1	32	-21.07	-29.07	23.01	HIS	CE1	32	-20.56	-20.56	24.17
HIS	NE2	32	-21.42	-28.84	25.02	HIS	C	32	-22.92	-22.92	20.64
HIS	O	32	-22.48	-30.94	21.16	ILE	N	33	-22.51	-22.51	19.47
ILE	CA	33	-21.41	-30.08	18.78	ILE	CB	33	-21.92	-21.92	17.47
ILE	CG2	33	-23.41	-31.12	17.27	ILE	CG1	33	-21.57	-21.57	16.25
ILE	CD1	33	-20.20	-30.72	15.72	ILE	C	33	-20.51	-20.51	18.49
ILE	O	33	-20.99	-27.83	18.00	ARG	N	34	-19.24	-19.24	18.89
ARG	CA	34	-18.32	-27.76	18.55	ARG	CB	34	-17.69	-17.69	19.81
ARG	CG	34	-18.74	-26.44	20.52	ARG	CD	34	-18.73	-18.73	21.99
ARG	NE	34	-17.76	-25.75	22.64	ARG	CZ	34	-16.93	-16.93	23.57
ARG	NH1	34	-16.03	-25.49	24.21	ARG	NH2	34	-16.93	-16.93	23.85
ARG	C	34	-17.21	-28.23	17.60	ARG	O	34	-16.93	-16.93	17.53
VAL	N	35	-16.55	-27.39	16.81	VAL	CA	35	-15.51	-15.51	15.90
VAL	CB	35	-15.93	-27.51	14.48	VAL	CG1	35	-14.97	-14.97	13.57
VAL	CG2	35	-17.30	-28.05	14.14	VAL	C	35	-14.26	-14.26	16.26
VAL	O	35	-14.39	-25.79	16.45	LEU	N	36	-13.05	-13.05	16.39
LEU	CA	36	-11.88	-26.80	16.77	LEU	CB	36	-10.59	-10.59	16.97
LEU	CG	36	-9.77	-27.74	18.26	LEU	CD1	36	-8.33	-8.33	17.85
LEU	CD2	36	-9.94	-26.65	19.25	LEU	C	36	-11.51	-11.51	15.62
LEU	O	36	-11.85	-26.20	14.47	GLN	N	37	-10.84	-10.84	15.81
GLN	CA	37	-10.26	-23.98	14.73	GLN	CB	37	-9.65	-9.65	15.28
GLN	CG	37	-8.57	-22.82	16.32	GLN	CD	37	-7.59	-7.59	16.16
GLN	OE1	37	-7.42	-20.76	16.96	GLN	NE2	37	-6.95	-6.95	14.99
GLN	C	37	-9.19	-24.83	14.03	GLN	O	37	-8.80	-8.80	14.54

FIG. 1·3

ARG	N	38	-8.81	-24.50	12.80	:	ARG	CA	38	-7.82	-7.82	12.03
ARG	CB	38	-7.59	-24.77	10.65	:	ARG	CG	38	-8.76	-8.76	9.82
ARG	CD	38	-8.49	-25.08	8.54	:	ARG	NE	38	-8.67	-8.67	7.42
ARG	CZ	38	-7.62	-23.92	6.68	:	ARG	NH1	38	-7.84	-7.84	5.64
ARG	NH2	38	-6.40	-24.37	6.96	:	ARG	C	38	-6.46	-6.46	12.64
ARG	O	38	-6.11	-24.14	13.08	:	PHE	N	39	-5.63	-5.63	12.64
PHE	CA	39	-4.31	-26.18	13.23	:	PHE	CB	39	-3.68	-3.68	13.35
PHE	CG	39	-4.49	-28.49	14.22	:	PHE	CD1	39	-4.59	-4.59	15.58
PHE	CD2	39	-5.10	-29.58	13.67	:	PHE	CE1	39	-5.28	-5.28	16.34
PHE	CE2	39	-5.80	-30.47	14.44	:	PHE	CZ	39	-5.89	-5.89	15.78
PHE	C	39	-3.39	-25.31	12.41	:	PHE	O	39	-2.72	-2.72	13.01
ASP	N	40	-3.28	-25.35	11.09	:	ASP	CA	40	-2.37	-2.37	10.35
ASP	CB	40	-2.12	-25.10	8.97	:	ASP	CG	40	-3.36	-3.36	8.12
ASP	OD1	40	-4.42	-25.50	8.54	:	ASP	OD2	40	-3.32	-3.32	7.05
ASP	C	40	-2.92	-23.07	10.27	:	ASP	O	40	-2.17	-2.17	10.03
GLN	N	41	-4.18	-22.75	10.44	:	GLN	CA	41	-4.61	-4.61	10.65
GLN	CB	41	-6.09	-21.15	10.99	:	GLN	CG	41	-6.70	-6.70	10.03
GLN	CD	41	-6.79	-20.69	8.57	:	GLN	OE1	41	-5.81	-5.81	7.87
GLN	NE2	41	-8.01	-20.84	8.01	:	GLN	C	41	-3.95	-3.95	11.88
GLN	O	41	-3.75	-19.62	11.98	:	GLN	N	42	-3.69	-3.69	12.89
GLN	CA	42	-3.12	-21.09	14.10	:	GLN	CB	42	-3.40	-3.40	15.16
GLN	CG	42	-3.74	-21.17	16.29	:	GLN	CD	42	-3.06	-3.06	17.58
GLN	OE1	42	-3.57	-21.23	18.66	:	GLN	NE2	42	-1.90	-1.90	17.48
GLN	C	42	-1.65	-20.83	14.03	:	GLN	O	42	-1.15	-1.15	14.70
SER	N	43	-0.91	-21.60	13.28	:	SER	CA	43	0.53	0.53	13.15
SER	CB	43	1.20	-22.10	14.34	:	SER	OG	43	2.53	2.53	14.44
SER	C	43	0.93	-22.23	11.90	:	SER	O	43	0.60	0.60	11.85
LYS	N	44	1.63	-21.73	10.89	:	LYS	CA	44	2.00	2.00	9.81
LYS	CB	44	2.54	-21.89	8.55	:	LYS	CG	44	1.57	1.57	7.30
LYS	CD	44	0.61	-23.38	7.21	:	LYS	CE	44	0.14	0.14	5.83
LYS	NZ	44	-0.82	-25.21	5.93	:	LYS	C	44	3.06	3.06	10.32
LYS	O	44	3.42	-24.51	9.60	:	ARG	N	45	3.55	3.55	11.58
ARG	CA	45	4.42	-24.48	12.14	:	ARG	CB	45	4.86	4.86	13.55
ARG	CG	45	5.34	-22.96	13.90	:	ARG	CD	45	5.97	5.97	15.24
ARG	NE	45	6.53	-21.95	15.79	:	ARG	CZ	45	7.50	7.50	16.70
ARG	NH1	45	7.91	-20.90	17.29	:	ARG	NH2	45	8.14	8.14	16.95
ARG	C	45	3.58	-25.73	12.24	:	ARG	O	45	4.11	4.11	12.07
LEU	N	46	2.27	-25.71	12.50	:	LEU	CA	46	1.49	1.49	12.63
LEU	CB	46	0.35	-26.72	13.61	:	LEU	CG	46	0.82	0.82	14.97
LEU	CD1	46	-0.32	-25.71	15.73	:	LEU	CD2	46	1.45	1.45	15.57
LEU	C	46	0.92	-27.25	11.29	:	LEU	O	46	-0.18	-0.18	11.21
GLN	N	47	1.68	-27.00	10.23	:	GLN	CA	47	1.24	1.24	8.85
GLN	CB	47	2.29	-26.70	7.94	:	GLN	CG	47	2.40	2.40	6.62
GLN	CD	47	3.30	-26.44	5.80	:	GLN	OE1	47	3.17	3.17	5.89
GLN	NE2	47	4.19	-27.04	4.99	:	GLN	C	47	0.90	0.90	8.48
GLN	O	47	-0.08	-28.81	7.80	:	ASN	N	48	1.70	1.70	8.82
ASN	CA	48	1.32	-30.94	8.49	:	ASN	CB	48	2.51	2.51	8.77
ASN	CG	48	3.46	-31.75	7.59	:	ASN	OD1	48	4.39	4.39	7.54
ASN	ND2	48	3.35	-30.92	6.56	:	ASN	C	48	0.09	0.09	9.19
ASN	O	48	-0.28	-32.65	9.00	:	LEU	N	49	-0.62	-0.62	9.96
LEU	CA	49	-1.82	-31.14	10.59	:	LEU	CB	49	-1.76	-1.76	12.01
LEU	CG	49	-1.80	-31.74	13.09	:	LEU	CD1	49	-1.09	-1.09	12.69
LEU	CD2	49	-1.14	-31.18	14.30	:	LEU	C	49	-2.87	-2.87	9.81
LEU	O	49	-3.92	-30.23	10.38	:	GLU	N	50	-2.80	-2.80	8.53
GLU	CA	50	-3.82	-29.18	7.92	:	GLU	CB	50	-3.15	-3.15	6.80
GLU	CG	50	-3.92	-27.75	5.68	:	GLU	CD	50	-3.02	-3.02	4.48
GLU	OE1	50	-3.35	-26.28	3.88	:	GLU	OE2	50	-1.97	-1.97	4.19
GLU	C	50	-5.01	-29.96	7.47	:	GLU	O	50	-6.14	-6.14	7.44
ASP	N	51	-4.78	-31.25	7.31	:	ASP	CA	51	-5.81	-5.81	6.88

FIG. 1.4.

ASP CB	51	-5.21	-33.38	6.26	:	ASP CG	51	-4.26	-4.26	5.11
ASP OD1	51	-4.68	-32.36	4.21	:	ASP OD2	51	-3.13	-3.13	5.12
ASP C	51	-6.64	-32.67	8.05	:	ASP O	51	-7.47	-7.47	7.84
TYR N	52	-6.48	-32.28	9.31	:	TYR CA	52	-7.23	-7.23	10.37
TYR CB	52	-6.35	-33.60	11.31	:	TYR CG	52	-5.58	-5.58	10.63
TYR CD1	52	-6.01	-35.97	10.64	:	TYR CE1	52	-5.26	-5.26	10.04
TYR CD2	52	-4.41	-34.37	10.01	:	TYR CE2	52	-3.65	-3.65	9.41
TYR CZ	52	-4.08	-36.63	9.44	:	TYR OH	52	-3.31	-3.31	8.87
TYR C	52	-8.01	-31.94	11.14	:	TYR O	52	-7.57	-7.57	11.23
ARG N	53	-9.18	-32.31	11.63	:	ARG CA	53	-9.95	-9.95	12.48
ARG CB	53	-11.20	-30.94	11.82	:	ARG CG	53	-10.97	-10.97	10.52
ARG CD	53	-10.20	-28.99	10.71	:	ARG NE	53	-11.08	-11.08	10.16
ARG CZ	53	-11.71	-27.11	10.92	:	ARG NH1	53	-12.62	-12.62	10.40
ARG NH2	53	-11.34	-26.97	12.18	:	ARG C	53	-10.39	-10.39	13.68
ARG O	53	-10.49	-33.40	13.59	:	LEU N	54	-10.69	-10.69	14.82
LEU CA	54	-11.18	-32.37	15.95	:	LEU CB	54	-10.49	-10.49	17.21
LEU CG	54	-9.16	-32.50	17.67	:	LEU CD1	54	-8.80	-8.80	18.94
LEU CD2	54	-9.23	-33.94	18.03	:	LEU C	54	-12.60	-12.60	16.05
LEU O	54	-12.77	-30.67	15.94	:	VAL N	55	-13.67	-13.67	16.15
VAL CA	55	-14.98	-32.07	16.45	:	VAL CB	55	-15.94	-15.94	15.18
VAL CG1	55	-15.35	-32.84	14.04	:	VAL CG2	55	-17.26	-17.26	15.53
VAL C	55	-15.54	-32.84	17.66	:	VAL O	55	-15.45	-15.45	17.68
GLU N	56	-16.10	-32.14	18.67	:	GLU CA	56	-16.47	-16.47	19.99
GLU CB	56	-15.64	-31.75	20.92	:	GLU CG	56	-16.00	-16.00	22.37
GLU CD	56	-17.12	-30.40	22.55	:	GLU OE1	56	-17.85	-17.85	23.55
GLU OE2	56	-17.28	-29.52	21.73	:	GLU C	56	-17.97	-17.97	20.17
GLU O	56	-18.56	-31.67	19.53	:	PHE N	57	-18.66	-18.66	20.98
PHE CA	57	-20.12	-33.36	21.06	:	PHE CB	57	-20.69	-20.69	20.13
PHE CG	57	-22.15	-34.85	20.30	:	PHE CD1	57	-22.47	-22.47	20.95
PHE CD2	57	-23.20	-34.13	19.74	:	PHE CE1	57	-23.79	-23.79	21.01
PHE CE2	57	-24.52	-34.54	19.80	:	PHE CZ	57	-24.82	-24.82	20.44
PHE C	57	-20.49	-33.75	22.45	:	PHE O	57	-19.78	-19.78	22.97
ARG N	58	-21.54	-33.24	23.07	:	ARG CA	58	-22.03	-22.03	24.32
ARG CB	58	-21.52	-33.05	25.54	:	ARG CG	58	-22.43	-22.43	26.44
ARG CD	58	-22.44	-32.83	27.83	:	ARG NE	58	-21.29	-21.29	28.65
ARG CZ	58	-21.23	-32.75	29.99	:	ARG NH1	58	-20.14	-20.14	30.71
ARG NH2	58	-22.26	-33.31	30.65	:	ARG C	58	-23.51	-23.51	24.26
ARG O	58	-23.97	-32.66	23.69	:	SER N	59	-24.26	-24.26	24.84
SER CA	59	-25.70	-34.48	24.82	:	SER CB	59	-26.24	-26.24	23.60
SER OG	59	-25.92	-36.63	23.38	:	SER C	59	-26.21	-26.21	26.12
SER O	59	-25.56	-35.97	26.72	:	LYS N	60	-27.36	-27.36	26.58
LYS CA	60	-27.95	-35.01	27.84	:	LYS CB	60	-29.05	-29.05	28.11
LYS CG	60	-28.58	-32.53	27.99	:	LYS CD	60	-28.62	-28.62	29.24
LYS CE	60	-28.33	-32.42	30.58	:	LYS NZ	60	-27.17	-27.17	30.57
LYS C	60	-28.47	-36.48	27.77	:	LYS O	60	-28.50	-28.50	26.67
PRO N	61	-28.82	-37.21	28.84	:	PRO CD	61	-28.43	-28.43	30.20
PRO CA	61	-29.53	-38.49	28.85	:	PRO CB	61	-30.02	-30.02	30.22
PRO CG	61	-28.81	-38.18	30.92	:	PRO C	61	-30.66	-30.66	27.87
PRO O	61	-31.36	-37.70	27.57	:	GLU N	62	-30.84	-30.84	27.42
GLU CA	62	-31.89	-40.28	26.47	:	GLU CB	62	-33.19	-33.19	27.26
GLU CG	62	-32.93	-41.46	28.44	:	GLU CD	62	-34.16	-34.16	29.02
GLU OE1	62	-34.25	-43.38	29.02	:	GLU OE2	62	-35.03	-35.03	29.49
GLU C	62	-32.07	-39.25	25.37	:	GLU O	62	-33.08	-33.08	25.26
THR N	63	-31.07	-39.08	24.51	:	THR CA	63	-31.17	-31.17	23.50
THR CB	63	-30.28	-36.96	24.10	:	THR OG1	63	-30.78	-30.78	23.73
THR CG2	63	-28.84	-37.20	23.71	:	THR C	63	-30.77	-30.77	22.14
THR O	63	-30.02	-39.56	22.14	:	LEU N	64	-31.22	-31.22	20.97
LEU CA	64	-30.75	-38.64	19.68	:	LEU CB	64	-31.87	-31.87	18.98
LEU CG	64	-31.85	-39.57	17.47	:	LEU CD1	64	-31.67	-31.67	17.07

FIG. 1.5.

LEU	CD2	64	-33.14	-39.04	16.91	:	LEU	C	64	-30.34	-30.34	18.82
LEU	O	64	-30.94	-36.37	18.89	:	LEU	N	65	-29.24	-29.24	18.08
LEU	CA	65	-28.80	-36.62	17.12	:	LEU	CB	65	-27.28	-27.28	17.14
LEU	CG	65	-26.49	-35.91	16.09	:	LEU	CD1	65	-26.66	-26.66	16.27
LEU	CD2	65	-25.06	-36.34	16.20	:	LEU	C	65	-29.43	-29.43	15.79
LEU	O	65	-29.30	-38.24	15.47	:	LEU	N	66	-30.21	-30.21	15.06
LEU	CA	66	-30.87	-36.62	13.82	:	LEU	CB	66	-31.81	-31.81	13.47
LEU	CG	66	-32.99	-35.29	14.43	:	LEU	CD1	66	-33.71	-33.71	14.12
LEU	CD2	66	-33.97	-36.44	14.28	:	LEU	C	66	-29.95	-29.95	12.65
LEU	O	66	-28.78	-36.57	12.70	:	PRO	N	67	-30.38	-30.38	11.60
PRO	CD	67	-31.65	-38.37	11.53	:	PRO	CA	67	-29.51	-29.51	10.53
PRO	CB	67	-30.42	-38.92	9.64	:	PRO	CG	67	-31.33	-31.33	10.62
PRO	C	67	-28.69	-37.16	9.73	:	PRO	O	67	-29.27	-29.27	9.20
GLN	N	68	-27.38	-37.32	9.57	:	GLN	CA	68	-26.54	-26.54	8.70
GLN	CB	68	-25.81	-35.55	9.57	:	GLN	CG	68	-24.60	-24.60	10.22
GLN	CD	68	-24.11	-35.37	11.37	:	GLN	OE1	68	-24.18	-24.18	12.49
GLN	NE2	68	-23.63	-34.17	11.13	:	GLN	C	68	-25.51	-25.51	7.82
GLN	O	68	-25.41	-38.41	7.97	:	GLN	N	69	-24.76	-24.76	6.92
GLN	CA	69	-23.57	-37.19	6.28	:	GLN	CB	69	-23.47	-23.47	4.80
GLN	CG	69	-24.66	-37.75	4.14	:	GLN	CD	69	-25.24	-25.24	3.37
GLN	OE1	69	-24.53	-35.78	2.80	:	GLN	NE2	69	-26.56	-26.56	3.31
GLN	C	69	-22.47	-36.15	6.42	:	GLN	O	69	-22.77	-22.77	6.30
ALA	N	70	-21.20	-36.45	6.63	:	ALA	CA	70	-20.21	-20.21	6.66
ALA	CB	70	-19.41	-35.44	7.93	:	ALA	C	70	-19.24	-19.24	5.53
ALA	O	70	-18.97	-36.70	5.18	:	ASP	N	71	-18.64	-18.64	4.91
ASP	CA	71	-17.63	-34.86	3.92	:	ASP	CB	71	-17.43	-17.43	2.94
ASP	CG	71	-17.03	-32.37	3.54	:	ASP	OD1	71	-16.21	-16.21	2.95
ASP	OD2	71	-17.56	-32.02	4.58	:	ASP	C	71	-16.33	-16.33	4.61
ASP	O	71	-15.28	-34.87	4.06	:	ALA	N	72	-16.23	-16.23	5.70
ALA	CA	72	-14.96	-36.17	6.35	:	ALA	CB	72	-14.79	-14.79	7.50
ALA	C	72	-14.88	-37.54	6.91	:	ALA	O	72	-15.90	-15.90	7.39
GLU	N	73	-13.79	-38.27	6.96	:	GLU	CA	73	-13.71	-13.71	7.63
GLU	CB	73	-12.44	-40.11	7.17	:	GLU	CG	73	-11.95	-11.95	7.68
GLU	CD	73	-12.40	-42.58	6.80	:	GLU	OE1	73	-11.99	-11.99	7.22
GLU	OE2	73	-13.12	-42.37	5.77	:	GLU	C	73	-13.71	-13.71	9.14
GLU	O	73	-13.00	-38.37	9.53	:	LEU	N	74	-14.42	-14.42	10.05
LEU	CA	74	-14.55	-39.60	11.46	:	LEU	CB	74	-15.98	-15.98	11.78
LEU	CG	74	-16.55	-37.93	11.81	:	LEU	CD1	74	-15.97	-15.97	10.75
LEU	CD2	74	-18.02	-38.04	11.60	:	LEU	C	74	-14.09	-14.09	12.32
LEU	O	74	-14.51	-41.85	12.05	:	LEU	N	75	-13.21	-13.21	13.29
LEU	CA	75	-12.84	-41.55	14.24	:	LEU	CB	75	-11.35	-11.35	14.31
LEU	CG	75	-10.68	-42.43	15.40	:	LEU	CD1	75	-11.37	-11.37	15.82
LEU	CD2	75	-9.43	-42.91	14.82	:	LEU	C	75	-13.49	-13.49	15.46
LEU	O	75	-13.13	-39.88	15.96	:	LEU	N	76	-14.58	-14.58	15.82
LEU	CA	76	-15.55	-41.26	16.86	:	LEU	CB	76	-16.84	-16.84	16.40
LEU	CG	76	-18.23	-41.53	16.75	:	LEU	CD1	76	-18.44	-18.44	18.21
LEU	CD2	76	-18.48	-40.13	16.31	:	LEU	C	76	-14.95	-14.95	18.10
LEU	O	76	-14.58	-43.03	17.97	:	VAL	N	77	-14.79	-14.79	19.26
VAL	CA	77	-14.18	-41.82	20.47	:	VAL	CB	77	-12.78	-12.78	20.72
VAL	CG1	77	-12.27	-41.63	22.08	:	VAL	CG2	77	-11.83	-11.83	19.84
VAL	C	77	-15.01	-41.44	21.67	:	VAL	O	77	-15.33	-15.33	21.80
VAL	N	78	-15.37	-42.31	22.60	:	VAL	CA	78	-16.21	-16.21	23.68
VAL	CB	78	-17.25	-42.95	23.93	:	VAL	CG1	78	-18.19	-18.19	25.01
VAL	CG2	78	-18.12	-43.15	22.73	:	VAL	C	78	-15.44	-15.44	24.94
VAL	O	78	-14.84	-42.35	25.55	:	ARG	N	79	-15.30	-15.30	25.36
ARG	CA	79	-14.86	-39.95	26.71	:	ARG	CB	79	-14.43	-14.43	26.82
ARG	CG	79	-14.02	-37.74	25.58	:	ARG	CD	79	-14.70	-14.70	25.37
ARG	NE	79	-13.74	-35.32	25.50	:	ARG	CZ	79	-13.99	-13.99	25.33
ARG	NH1	79	-13.07	-33.09	25.61	:	ARG	NH2	79	-15.17	-15.17	24.82

FIG. 1.6.

ARG	C	79	-16.20	-40.10	27.50	:	ARG	O	79	-17.24	-17.24	26.90
SER	N	80	-16.49	-40.50	28.75	:	SER	CA	80	-17.91	-17.91	29.29
SER	CB	80	-18.40	-39.17	29.61	:	SER	OG	80	-17.56	-17.56	30.62
SER	C	80	-19.07	-41.27	28.53	:	SER	O	80	-19.95	-19.95	27.93
GLY	N	81	-18.96	-42.60	28.70	:	GLY	CA	81	-19.64	-19.64	28.06
GLY	C	81	-21.11	-43.61	27.77	:	GLY	O	81	-21.73	-21.73	28.31
SER	N	82	-21.62	-44.58	26.99	:	SER	CA	82	-23.00	-23.00	26.46
SER	CB	82	-23.92	-43.63	26.88	:	SER	OG	82	-23.45	-23.45	26.23
SER	C	82	-23.01	-44.67	24.89	:	SER	O	82	-22.00	-22.00	24.31
ALA	N	83	-23.96	-44.07	24.15	:	ALA	CA	83	-23.96	-23.96	22.68
ALA	CB	83	-22.71	-43.47	22.06	:	ALA	C	83	-24.11	-24.11	21.88
ALA	O	83	-23.33	-46.28	21.95	:	ILE	N	84	-25.16	-25.16	21.09
ILE	CA	84	-25.51	-46.45	20.19	:	ILE	CB	84	-26.99	-26.99	20.33
ILE	CG2	84	-27.43	-47.70	19.14	:	ILE	CG1	84	-27.19	-27.19	21.63
ILE	CD1	84	-28.67	-47.63	22.03	:	ILE	C	84	-25.32	-25.32	18.87
ILE	O	84	-25.98	-44.71	18.65	:	LEU	N	85	-24.51	-24.51	17.94
LEU	CA	85	-24.36	-45.46	16.70	:	LEU	CB	85	-22.90	-22.90	16.51
LEU	CG	85	-22.27	-44.83	15.24	:	LEU	CD1	85	-22.67	-22.67	14.86
LEU	CD2	85	-20.78	-45.01	15.45	:	LEU	C	85	-24.93	-24.93	15.64
LEU	O	85	-24.79	-47.57	15.74	:	VAL	N	86	-25.60	-25.60	14.65
VAL	CA	86	-26.00	-46.71	13.56	:	VAL	CB	86	-27.56	-27.56	13.57
VAL	CG1	86	-28.28	-46.04	14.42	:	VAL	CG2	86	-28.15	-28.15	12.19
VAL	C	86	-25.55	-46.05	12.27	:	VAL	O	86	-25.74	-25.74	12.14
LEU	N	87	-24.88	-46.77	11.38	:	LEU	CA	87	-24.55	-24.55	10.11
LEU	CB	87	-23.25	-46.65	9.61	:	LEU	CG	87	-22.11	-22.11	10.54
LEU	CD1	87	-20.93	-47.07	9.70	:	LEU	CD2	87	-21.85	-21.85	11.28
LEU	C	87	-25.66	-46.73	9.22	:	LEU	O	87	-26.00	-26.00	9.39
VAL	N	88	-26.30	-45.98	8.31	:	VAL	CA	88	-27.35	-27.35	7.46
VAL	CB	88	-28.47	-45.49	7.41	:	VAL	CG1	98	-29.45	-29.45	6.38
VAL	CG2	88	-29.12	-45.33	8.76	:	VAL	C	88	-26.69	-26.69	6.11
VAL	O	88	-26.15	-45.62	5.66	:	LYS	N	89	-26.65	-26.65	5.38
LYS	CA	89	-25.94	-47.80	4.10	:	LYS	CB	89	-25.02	-25.02	4.15
LYS	CG	89	-23.71	-48.54	4.77	:	LYS	CD	89	-22.73	-22.73	5.27
LYS	CE	89	-21.54	-48.85	5.96	:	LYS	NZ	89	-20.87	-20.87	7.05
LYS	C	89	-26.98	-47.86	2.97	:	LYS	O	89	-28.07	-28.07	3.24
PRO	N	90	-26.80	-47.35	1.74	:	PRO	CD	90	-25.54	-25.54	1.17
PRO	CA	90	-27.81	-47.17	0.73	:	PRO	CB	90	-27.18	-27.18	-0.39
PRO	CG	90	-25.82	-46.96	-0.33	:	PRO	C	90	-28.36	-28.36	0.26
PRO	O	90	-29.58	-48.64	0.08	:	ASP	N	91	-27.55	-27.55	0.14
ASP	CA	91	-28.01	-50.83	-0.22	:	ASP	CB	91	-26.81	-26.81	-0.70
ASP	CG	91	-25.71	-51.69	0.33	:	ASP	OD1	91	-25.45	-25.45	1.04
ASP	OD2	91	-25.10	-52.76	0.44	:	ASP	C	91	-28.68	-28.68	0.95
ASP	O	91	-28.25	-52.60	1.40	:	ASP	N	92	-29.73	-29.73	1.52
ASP	CA	92	-30.47	-51.44	2.66	:	ASP	CB	92	-31.47	-31.47	2.22
ASP	CG	92	-32.80	-52.49	2.95	:	ASP	OD1	92	-33.66	-33.66	2.43
ASP	OD2	92	-33.06	-51.80	3.97	:	ASP	C	92	-29.68	-29.68	3.77
ASP	O	92	-30.30	-52.74	4.60	:	ARG	N	93	-28.36	-28.36	3.91
ARG	CA	93	-27.71	-52.49	5.11	:	ARG	CB	93	-26.24	-26.24	4.79
ARG	CG	93	-25.90	-53.91	3.68	:	ARG	CD	93	-24.33	-24.33	3.58
ARG	NE	93	-23.80	-54.65	4.89	:	ARG	CZ	93	-23.11	-23.11	5.89
ARG	NH1	93	-22.86	-54.55	7.10	:	ARG	NH2	93	-22.59	-22.59	5.67
ARG	C	93	-27.82	-51.43	6.22	:	ARG	O	93	-28.34	-28.34	6.03
ARG	N	94	-27.38	-51.77	7.43	:	ARG	CA	94	-27.28	-27.28	8.64
ARG	CB	94	-28.49	-51.02	9.53	:	ARG	CG	94	-29.32	-29.32	9.54
ARG	CD	94	-30.26	-49.70	8.35	:	ARG	NE	94	-31.09	-31.09	8.24
ARG	CZ	94	-31.62	-51.29	7.06	:	ARG	NH1	94	-32.34	-32.34	6.95
ARG	NH2	94	-31.49	-50.56	5.96	:	ARG	C	94	-26.14	-26.14	9.46
ARG	O	94	-25.65	-52.66	9.15	:	GLU	N	95	-25.69	-25.69	10.48
GLU	CA	95	-24.63	-51.38	11.31	:	GLU	CB	95	-23.30	-23.30	10.84

FIG. 1.7.

GLU	CG	95	-22.38	-52.01	10.37	:	GLU	CD	95	-21.96	-21.96	8.93
GLU	OE1	95	-20.79	-51.95	8.57	:	GLU	OE2	95	-22.78	-22.78	8.07
GLU	C	95	-24.95	-50.70	12.61	:	GLU	O	95	-25.21	-25.21	12.58
TYR	N	96	-24.98	-51.44	13.73	:	TYR	CA	96	-25.32	-25.32	15.06
TYR	CB	96	-26.41	-51.68	15.76	:	TYR	CG	96	-27.66	-27.66	14.92
TYR	CD1	96	-28.61	-50.70	15.19	:	TYR	CE1	96	-29.68	-29.68	14.35
TYR	CD2	96	-27.76	-52.44	13.82	:	TYR	CE2	96	-28.81	-28.81	12.98
TYR	CZ	96	-29.76	-51.34	13.24	:	TYR	OH	96	-30.78	-30.78	12.33
TYR	C	96	-24.06	-51.07	15.88	:	TYR	O	96	-23.50	-23.50	15.91
PHE	N	97	-23.49	-50.03	16.46	:	PHE	CA	97	-22.41	-22.41	17.38
PHE	CB	97	-21.24	-49.51	17.00	:	PHE	CG	97	-20.75	-20.75	15.64
PHE	CD1	97	-21.31	-49.23	14.59	:	PHE	CD2	97	-19.75	-19.75	15.50
PHE	CE1	97	-20.82	-49.51	13.36	:	PHE	CE2	97	-19.27	-19.27	14.27
PHE	CZ	97	-19.81	-50.43	13.20	:	PHE	C	97	-22.88	-22.88	18.70
PHE	O	97	-23.58	-48.66	18.77	:	PHE	N	98	-22.55	-22.55	19.80
PHE	CA	98	-22.81	-49.88	21.13	:	PHE	CB	98	-23.49	-23.49	21.97
PHE	CG	98	-23.71	-50.44	23.39	:	PHE	CD1	98	-24.78	-24.78	23.67
PHE	CD2	98	-22.85	-50.81	24.41	:	PHE	CE1	98	-24.98	-24.98	24.96
PHE	CE2	98	-23.04	-50.38	25.70	:	PHE	CZ	98	-24.12	-24.12	25.97
PHE	C	98	-21.37	-49.65	21.57	:	PHE	O	98	-20.53	-20.53	21.59
LEU	N	99	-21.13	-48.36	21.70	:	LEU	CA	99	-19.85	-19.85	22.04
LEU	CB	99	-19.68	-46.53	21.20	:	LEU	CG	99	-18.81	-18.81	19.97
LEU	CD1	99	-19.04	-47.67	19.14	:	LEU	CD2	99	-19.12	-19.12	19.19
LEU	C	99	-19.93	-47.49	23.54	:	LEU	O	99	-21.02	-21.02	24.08
THR	N	100	-18.86	-47.28	24.29	:	THR	CA	100	-18.87	-18.87	25.67
THR	CB	100	-19.58	-47.78	26.62	:	THR	OG1	100	-19.74	-19.74	27.76
THR	CG2	100	-18.88	-49.07	27.01	:	THR	C	100	-17.42	-17.42	26.16
THR	O	100	-16.60	-47.53	25.72	:	SER	N	101	-17.13	-17.13	27.10
SER	CA	101	-15.75	-45.57	27.49	:	SER	CB	101	-15.63	-15.63	28.52
SER	OG	101	-16.16	-44.81	29.79	:	SER	C	101	-15.00	-15.00	28.07
SER	O	101	-15.63	-47.76	28.43	:	ASP	N	102	-13.66	-13.66	28.11
ASP	CA	102	-12.69	-47.42	28.83	:	ASP	CB	102	-12.75	-12.75	30.25
ASP	CG	102	-13.60	-47.61	31.27	:	ASP	OD1	102	-14.77	-14.77	30.97
ASP	OD2	102	-13.01	-47.94	32.32	:	ASP	C	102	-12.83	-12.83	28.77
ASP	O	102	-12.99	-49.56	27.67	:	ASN	N	103	-12.59	-12.59	29.88
ASN	CA	103	-12.92	-51.11	30.03	:	ASN	CB	103	-12.58	-12.58	31.45
ASN	CG	103	-13.56	-50.80	32.49	:	ASN	OD1	103	-13.21	-13.21	33.68
ASN	ND2	103	-14.73	-50.15	32.37	:	ASN	C	103	-14.40	-14.40	29.72
ASN	O	103	-15.33	-50.69	29.83	:	PRO	N	104	-14.72	-14.72	29.51
PRO	CD	104	-15.18	-53.63	30.64	:	PRO	CA	104	-14.17	-14.17	28.44
PRO	CB	104	-13.35	-54.64	29.25	:	PRO	CG	104	-14.34	-14.34	30.42
PRO	C	104	-15.33	-54.33	27.65	:	PRO	O	104	-16.50	-16.50	27.93
ILE	N	105	-15.07	-55.33	26.75	:	ILE	CA	105	-16.08	-16.08	25.86
ILE	CB	105	-16.66	-57.27	26.63	:	ILE	CG2	105	-17.34	-17.34	27.98
ILE	CG1	105	-17.66	-58.03	25.68	:	ILE	CD1	105	-17.03	-17.03	24.74
ILE	C	105	-17.21	-55.05	25.35	:	ILE	O	105	-18.41	-18.41	25.61
PHE	N	106	-16.74	-53.92	24.75	:	PHE	CA	106	-17.58	-17.58	24.07
PHE	CB	106	-18.48	-52.14	25.06	:	PHE	CG	106	-19.83	-19.83	25.17
PHE	CD1	106	-20.28	-53.69	24.14	:	PHE	CD2	106	-20.57	-20.57	26.33
PHE	CE1	106	-21.47	-54.41	24.27	:	PHE	CE2	106	-21.75	-21.75	26.45
PHE	CZ	106	-22.21	-54.28	25.44	:	PHE	C	106	-16.93	-16.93	23.13
PHE	O	106	-17.52	-51.66	22.05	:	SER	N	107	-15.73	-15.73	23.38
SER	CA	107	-15.09	-50.38	22.50	:	SER	CB	107	-15.18	-15.18	20.98
SER	OG	107	-14.04	-50.06	20.37	:	SER	C	107	-15.70	-15.70	22.67
SER	O	107	-16.90	-48.77	22.83	:	ASP	N	108	-14.70	-14.70	22.76
ASP	CA	108	-14.95	-46.76	22.94	:	ASP	CB	108	-14.05	-14.05	24.02
ASP	CG	108	-12.55	-46.26	23.80	:	ASP	OD1	108	-11.87	-11.87	24.62
ASP	OD2	108	-12.00	-46.87	22.86	:	ASP	C	108	-14.74	-14.74	21.65
ASP	O	108	-14.81	-44.84	21.62	:	HIS	N	109	-14.51	-14.51	20.54

FIG. 1·8.

HIS	CA	109	-14.47	-45.96	19.31	:	HIS	CB	109	-13.14	-13.14	18.95
HIS	CG	109	-12.21	-46.61	19.00	:	HIS	CD2	109	-11.61	-11.61	17.95
HIS	ND1	109	-11.80	-47.13	20.13	:	HIS	CE1	109	-10.92	-10.92	19.84
HIS	NE2	109	-10.81	-48.11	18.52	:	HIS	C	109	-14.94	-14.94	18.07
HIS	O	109	-15.10	-47.83	18.08	:	GLN	N	110	-15.06	-15.06	16.97
GLN	CA	110	-15.62	-46.48	15.78	:	GLN	CB	110	-17.11	-17.11	16.04
GLN	CG	110	-17.80	-47.48	14.97	:	GLN	CD	110	-17.02	-17.02	14.40
GLN	OE1	110	-16.83	-48.73	13.20	:	GLN	NE2	110	-16.49	-16.49	15.14
GLN	C	110	-15.33	-45.49	14.67	:	GLN	O	110	-15.29	-15.29	14.92
LYS	N	111	-15.06	-45.99	13.48	:	LYS	CA	111	-14.74	-14.74	12.34
LYS	CB	111	-13.62	-45.88	11.64	:	LYS	CG	111	-13.16	-13.16	10.33
LYS	CD	111	-12.32	-46.31	9.49	:	LYS	CE	111	-11.20	-11.20	10.35
LYS	NZ	111	-9.93	-47.28	9.70	:	LYS	C	111	-15.99	-15.99	11.48
LYS	O	111	-16.47	-46.07	10.95	:	ILE	N	112	-16.58	-16.58	11.34
ILE	CA	112	-17.76	-43.75	10.51	:	ILE	CB	112	-18.60	-18.60	11.06
ILE	CG2	112	-19.90	-42.58	10.27	:	ILE	CG1	112	-18.83	-18.83	12.53
ILE	CD1	112	-19.66	-41.59	13.03	:	ILE	C	112	-17.18	-17.18	9.13
ILE	O	112	-16.49	-42.41	9.10	:	PRO	N	113	-17.31	-17.31	7.98
PRO	CD	113	-18.03	-45.26	7.79	:	PRO	CA	113	-16.49	-16.49	6.82
PRO	CB	113	-16.58	-44.96	6.01	:	PRO	CG	113	-17.03	-17.03	6.98
PRO	C	113	-16.94	-42.47	6.08	:	PRO	O	113	-18.13	-18.13	6.09
ALA	N	114	-16.15	-41.73	5.35	:	ALA	CA	114	-16.62	-16.62	4.74
ALA	CB	114	-15.47	-39.96	3.92	:	ALA	C	114	-17.91	-17.91	3.92
ALA	O	114	-17.91	-40.47	2.70	:	GLY	N	115	-19.07	-19.07	4.50
GLY	CA	115	-20.23	-39.80	3.73	:	GLY	C	115	-21.33	-21.33	4.04
GLY	O	115	-22.33	-40.62	3.36	:	THR	N	116	-21.16	-21.16	5.00
THR	CA	116	-22.15	-42.66	5.54	:	THR	CB	116	-21.62	-21.62	6.54
THR	OG1	116	-20.35	-44.09	6.13	:	THR	CG2	116	-22.37	-22.37	6.51
THR	C	116	-23.11	-41.88	6.39	:	THR	O	116	-22.63	-22.63	7.11
ILE	N	117	-24.40	-42.15	6.31	:	ILE	CA	117	-25.35	-25.35	7.14
ILE	CB	117	-26.70	-41.56	6.42	:	ILE	CG2	117	-27.84	-27.84	7.40
ILE	CG1	117	-26.83	-40.39	5.47	:	ILE	CD1	117	-28.22	-28.22	4.94
ILE	C	117	-25.33	-42.10	8.52	:	ILE	O	117	-25.25	-25.25	8.59
PHE	N	118	-25.40	-41.42	9.65	:	PHE	CA	118	-25.34	-25.34	10.93
PHE	CB	118	-23.88	-42.14	11.46	:	PHE	CG	118	-23.14	-23.14	11.78
PHE	CD1	118	-23.21	-40.33	13.06	:	PHE	CD2	118	-22.47	-22.47	10.81
PHE	CE1	118	-22.61	-39.14	13.35	:	PHE	CE2	118	-21.87	-21.87	11.12
PHE	CZ	118	-21.94	-38.47	12.38	:	PHE	C	118	-26.24	-26.24	11.90
PHE	O	118	-26.40	-40.18	11.74	:	TYR	N	119	-26.89	-26.89	12.87
TYR	CA	119	-27.52	-41.17	13.89	:	TYR	CB	119	-29.07	-29.07	13.80
TYR	CG	119	-29.81	-42.53	13.49	:	TYR	CD1	119	-29.75	-29.75	12.23
TYR	CE1	119	-30.40	-44.23	12.00	:	TYR	CD2	119	-30.50	-30.50	14.50
TYR	CE2	119	-31.15	-44.38	14.27	:	TYR	CZ	119	-31.08	-31.08	13.00
TYR	OH	119	-31.57	-46.13	12.70	:	TYR	C	119	-27.01	-27.01	15.20
TYR	O	119	-26.45	-42.78	15.23	:	LEU	N	120	-27.11	-27.11	16.31
LEU	CA	120	-26.42	-41.44	17.53	:	LEU	CB	120	-25.31	-25.31	17.83
LEU	CG	120	-23.86	-40.75	17.90	:	LEU	CD1	120	-23.09	-23.09	17.72
LEU	CD2	120	-23.50	-41.32	19.23	:	LEU	C	120	-27.47	-27.47	18.62
LEU	O	120	-28.22	-40.39	18.55	:	VAL	N	121	-27.70	-27.70	19.56
VAL	CA	121	-28.66	-41.97	20.61	:	VAL	CB	121	-29.94	-29.94	20.60
VAL	CG1	121	-30.11	-43.46	19.21	:	VAL	CG2	121	-29.89	-29.89	21.59
VAL	C	121	-27.88	-42.08	21.90	:	VAL	O	121	-26.85	-26.85	21.88
ASN	N	122	-28.22	-41.40	23.00	:	ASN	CA	122	-27.49	-27.49	24.27
ASN	CB	122	-27.36	-40.18	25.06	:	ASN	CG	122	-26.75	-26.75	26.48
ASN	OD1	122	-26.35	-41.42	26.91	:	ASN	ND2	122	-26.65	-26.65	27.33
ASN	C	122	-28.42	-42.42	25.04	:	ASN	O	122	-29.52	-29.52	25.43
ARG	N	123	-27.98	-43.66	25.22	:	ARG	CA	123	-28.84	-28.84	25.72
ARG	CB	123	-28.18	-45.97	25.51	:	ARG	CG	123	-26.78	-26.78	26.17
ARG	CD	123	-26.34	-46.96	27.34	:	ARG	NE	123	-26.83	-26.83	28.73

FIG. 1.9.

ARG	CZ	123	-27.92	-47.53	29.20	:	ARG	NH1	123	-28.26	-28.26	30.51
ARG	NH2	123	-28.69	-48.33	28.35	:	ARG	C	123	-29.16	-29.16	27.17
ARG	O	123	-29.99	-45.29	27.68	:	ASP	N	124	-28.41	-28.41	27.89
ASP	CA	124	-28.41	-43.82	29.32	:	ASP	CB	124	-27.00	-27.00	29.66
ASP	CG	124	-26.82	-43.92	31.10	:	ASP	OD1	124	-27.09	-27.09	31.98
ASP	OD2	124	-26.50	-45.09	31.31	:	ASP	C	124	-29.33	-29.33	29.92
ASP	O	124	-29.39	-41.67	29.34	:	PRO	N	125	-30.06	-30.06	31.04
PRO	CD	125	-30.08	-44.21	31.82	:	PRO	CA	125	-31.11	-31.11	31.51
PRO	CB	125	-32.18	-43.01	31.95	:	PRO	CG	125	-31.31	-31.31	32.70
PRO	C	125	-30.60	-41.19	32.61	:	PRO	O	125	-31.38	-31.38	33.15
LYS	N	126	-29.29	-41.29	32.93	:	LYS	CA	126	-28.78	-28.78	33.91
LYS	CB	126	-28.84	-41.09	35.28	:	LYS	CG	126	-27.64	-27.64	36.08
LYS	CD	126	-26.81	-42.73	35.39	:	LYS	CE	126	-25.85	-25.85	36.36
LYS	NZ	126	-25.25	-42.56	37.35	:	LYS	C	126	-27.42	-27.42	33.54
LYS	O	126	-27.33	-38.50	33.61	:	GLU	N	127	-26.40	-26.40	33.07
GLU	CA	127	-25.14	-39.81	32.71	:	GLU	CB	127	-24.13	-24.13	32.94
GLU	CG	127	-23.20	-40.68	34.17	:	GLU	CD	127	-23.80	-23.80	35.61
GLU	OE1	127	-24.84	-39.90	35.86	:	GLU	OE2	127	-23.27	-23.27	36.56
GLU	C	127	-25.15	-39.17	31.28	:	GLU	O	127	-25.88	-25.88	30.39
ASP	N	128	-24.51	-38.01	30.97	:	ASP	CA	128	-24.42	-24.42	29.59
ASP	CB	128	-23.82	-36.04	29.56	:	ASP	CG	128	-24.72	-24.72	30.18
ASP	OD1	128	-24.75	-33.82	29.78	:	ASP	OD2	128	-25.42	-25.42	31.15
ASP	C	128	-23.55	-38.30	28.66	:	ASP	O	128	-22.91	-22.91	29.09
LEU	N	129	-23.48	-37.96	27.37	:	LEU	CA	129	-22.63	-22.63	26.39
LEU	CB	129	-23.33	-38.90	25.07	:	LEU	CG	129	-22.98	-22.98	24.13
LEU	CD1	129	-23.13	-39.52	22.75	:	LEU	CD2	129	-21.59	-21.59	24.30
LEU	C	129	-21.54	-37.63	26.09	:	LEU	O	129	-21.95	-21.95	25.88
ARG	N	130	-20.24	-37.98	26.09	:	ARG	CA	130	-19.26	-19.26	25.66
ARG	CB	130	-18.44	-36.57	26.87	:	ARG	CG	130	-19.22	-19.22	27.86
ARG	CD	130	-18.43	-34.73	28.70	:	ARG	NE	130	-17.26	-17.26	29.25
ARG	CZ	130	-16.05	-34.80	29.39	:	ARG	NH1	130	-15.10	-15.10	29.95
ARG	NH2	130	-15.64	-33.58	28.94	:	ARG	C	130	-18.36	-18.36	24.52
ARG	O	130	-17.39	-38.20	24.75	:	ILE	N	131	-18.52	-18.52	23.24
ILE	CA	131	-17.68	-37.73	22.17	:	ILE	CB	131	-18.61	-18.61	20.99
ILE	CG2	131	-17.86	-38.40	19.73	:	ILE	CG1	131	-19.50	-19.50	21.44
ILE	CD1	131	-20.52	-39.68	20.45	:	ILE	C	131	-16.58	-16.58	21.79
ILE	O	131	-16.80	-35.58	21.98	:	ILE	N	132	-15.42	-15.42	21.31
ILE	CA	132	-14.31	-36.36	20.82	:	ILE	CB	132	-13.06	-13.06	21.79
ILE	CG2	132	-12.38	-37.80	21.79	:	ILE	CG1	132	-11.95	-11.95	21.26
ILE	CD1	132	-12.16	-34.09	21.44	:	ILE	C	132	-14.02	-14.02	19.44
ILE	O	132	-14.06	-38.21	19.37	:	GLN	N	133	-13.77	-13.77	18.28
GLN	CA	133	-13.61	-37.13	17.05	:	GLN	CB	133	-14.76	-14.76	16.13
GLN	CG	133	-16.08	-37.06	16.81	:	GLN	CD	133	-17.25	-17.25	15.86
GLN	OE1	133	-17.14	-37.00	14.66	:	GLN	NE2	133	-18.47	-18.47	16.28
GLN	C	133	-12.46	-36.54	16.31	:	GLN	O	133	-12.25	-12.25	16.42
LEU	N	134	-11.69	-37.35	15.61	:	LEU	CA	134	-10.65	-10.65	14.76
LEU	CB	134	-9.42	-37.67	14.78	:	LEU	CG	134	-8.39	-8.39	13.77
LEU	CD1	134	-7.62	-36.10	14.11	:	LEU	CD2	134	-7.47	-7.47	13.73
LEU	C	134	-11.35	-36.91	13.42	:	LEU	O	134	-11.86	-11.86	13.10
ALA	N	135	-11.48	-35.87	12.63	:	ALA	CA	135	-12.19	-12.19	11.40
ALA	CB	135	-13.27	-34.89	11.39	:	ALA	C	135	-11.15	-11.15	10.34
ALA	O	135	-10.30	-34.77	10.58	:	MET	N	136	-11.13	-11.13	9.19
MET	CA	136	-10.17	-36.01	8.14	:	MET	CB	136	-9.42	-9.42	7.85
MET	CG	136	-8.72	-37.84	9.12	:	MET	SD	136	-8.72	-8.72	9.74
MET	CE	136	-10.20	-39.92	10.67	:	MET	C	136	-11.01	-11.01	6.95
MET	O	136	-11.64	-36.43	6.36	:	PRO	N	137	-11.22	-11.22	6.55
PRO	CD	137	-10.68	-33.11	7.14	:	PRO	CA	137	-12.14	-12.14	5.49
PRO	CB	137	-12.24	-32.44	5.61	:	PRO	CG	137	-11.86	-11.86	7.02
PRO	C	137	-11.66	-34.38	4.13	:	PRO	O	137	-10.47	-10.47	3.85

FIG. 1·10.

VAL	N	138	-12.58	-34.81	3.28	:	VAL	CA	138	-12.31	-12.31	1.95
VAL	CB	138	-13.48	-36.17	1.52	:	VAL	CG1	138	-13.40	-13.40	0.11
VAL	CG2	138	-13.41	-37.40	2.33	:	VAL	C	138	-12.06	-12.06	0.94
VAL	O	138	-11.28	-34.37	0.02	:	ASN	N	139	-12.78	-12.78	1.02
ASN	CA	139	-12.74	-31.94	0.07	:	ASN	CB	139	-14.11	-14.11	0.03
ASN	CG	139	-15.11	-32.24	-0.64	:	ASN	OD1	139	-16.26	-16.26	-0.25
ASN	ND2	139	-14.75	-32.85	-1.75	:	ASN	C	139	-11.75	-11.75	0.09
ASN	O	139	-11.19	-30.37	-0.93	:	ASN	N	140	-11.61	-11.61	1.24
ASN	CA	140	-10.74	-29.01	1.55	:	ASN	CB	140	-11.22	-11.22	0.98
ASN	CG	140	-12.71	-27.61	1.05	:	ASN	OD1	140	-13.29	-13.29	2.06
ASN	ND2	140	-13.44	-27.87	0.00	:	ASN	C	140	-10.77	-10.77	3.04
ASN	O	140	-11.72	-29.44	3.54	:	PRO	N	141	-9.98	-9.98	3.90
PRO	CD	141	-8.90	-27.39	3.54	:	PRO	CA	141	-9.86	-9.86	5.32
PRO	CB	141	-8.61	-27.99	5.78	:	PRO	CG	141	-8.55	-8.55	4.89
PRO	C	141	-11.01	-28.39	6.27	:	PRO	O	141	-10.91	-10.91	7.49
GLN	N	142	-12.13	-27.94	5.73	:	GLN	CA	142	-13.34	-13.34	6.45
GLN	CB	142	-14.15	-26.64	5.77	:	GLN	CG	142	-13.23	-13.23	5.02
GLN	CD	142	-13.43	-24.42	5.61	:	GLN	OE1	142	-14.56	-14.56	5.48
GLN	NE2	142	-12.42	-23.91	6.35	:	GLN	C	142	-14.21	-14.21	6.46
GLN	O	142	-14.32	-29.46	5.42	:	ILE	N	143	-14.88	-14.88	7.56
ILE	CA	143	-15.73	-30.31	7.60	:	ILE	CB	143	-15.46	-15.46	8.92
ILE	CG2	143	-15.41	-30.26	10.15	:	ILE	CG1	143	-16.57	-16.57	9.05
ILE	CD1	143	-16.22	-33.21	10.01	:	ILE	C	143	-17.14	-17.14	7.48
ILE	O	143	-17.39	-28.61	7.99	:	HIS	N	144	-18.00	-18.00	6.68
HIS	CA	144	-19.34	-29.88	6.45	:	HIS	CB	144	-19.58	-19.58	4.99
HIS	CG	144	-18.53	-28.73	4.36	:	HIS	CD2	144	-17.86	-17.86	3.31
HIS	ND1	144	-18.00	-27.57	4.68	:	HIS	CE1	144	-17.01	-17.01	3.88
HIS	NE2	144	-16.95	-28.35	3.06	:	HIS	C	144	-20.32	-20.32	6.87
HIS	O	144	-20.12	-32.15	6.57	:	GLU	N	145	-21.40	-21.40	7.54
GLU	CA	145	-22.39	-31.56	7.97	:	GLU	CB	145	-22.62	-22.62	9.36
GLU	CG	145	-21.61	-32.31	9.92	:	GLU	CD	145	-21.37	-21.37	11.38
GLU	OE1	145	-20.21	-32.02	11.80	:	GLU	OE2	145	-22.34	-22.34	12.11
GLU	C	145	-23.67	-31.35	7.24	:	GLU	O	145	-24.26	-24.26	7.25
PHE	N	146	-24.10	-32.39	6.57	:	PHE	CA	146	-25.31	-25.31	5.83
PHE	CB	146	-25.09	-32.99	4.51	:	PHE	CG	146	-24.19	-24.19	3.54
PHE	CD1	146	-22.83	-32.34	3.63	:	PHE	CD2	146	-24.76	-24.76	2.60
PHE	CE1	146	-22.04	-31.65	2.77	:	PHE	CE2	146	-23.96	-23.96	1.75
PHE	CZ	146	-22.61	-30.85	1.83	:	PHE	C	146	-26.38	-26.38	6.67
PHE	O	146	-26.43	-34.16	6.66	:	PHE	N	147	-27.24	-27.24	7.41
PHE	CA	147	-28.25	-32.85	8.20	:	PHE	CB	147	-28.77	-28.77	9.28
PHE	CG	147	-27.96	-32.05	10.55	:	PHE	CD1	147	-27.09	-27.09	10.91
PHE	CD2	147	-28.03	-33.19	11.31	:	PHE	CE1	147	-26.30	-26.30	12.03
PHE	CE2	147	-27.23	-33.35	12.42	:	PHE	CZ	147	-26.36	-26.36	12.78
PHE	C	147	-29.38	-33.14	7.26	:	PHE	O	147	-29.72	-29.72	6.46
LEU	N	148	-29.97	-34.33	7.29	:	LEU	CA	148	-31.14	-31.14	6.48
LEU	CB	148	-31.49	-36.11	6.51	:	LEU	CG	148	-31.58	-31.58	5.26
LEU	CD1	148	-32.43	-38.14	5.53	:	LEU	CD2	148	-32.29	-32.29	4.19
LEU	C	148	-32.38	-33.95	7.01	:	LEU	O	148	-33.33	-33.33	6.24
SER	N	149	-32.37	-33.56	8.29	:	SER	CA	149	-33.58	-33.58	8.92
SER	CB	149	-33.30	-33.21	10.40	:	SER	OG	149	-32.18	-32.18	10.87
SER	C	149	-34.53	-31.98	8.70	:	SER	O	149	-35.63	-35.63	8.79
SER	N	150	-34.58	-30.69	8.39	:	SER	CA	150	-35.84	-35.84	8.54
SER	CB	150	-37.05	-30.34	7.76	:	SER	OG	150	-37.23	-37.23	6.81
SER	C	150	-36.32	-29.80	10.00	:	SER	O	150	-36.99	-36.99	10.59
THR	N	151	-35.99	-28.67	10.62	:	THR	CA	151	-36.11	-36.11	12.06
THR	CB	151	-34.87	-28.95	12.85	:	THR	OG1	151	-33.85	-33.85	12.10
THR	CG2	151	-34.74	-30.43	13.15	:	THR	C	151	-36.46	-36.46	12.72
THR	O	151	-37.00	-27.46	13.80	:	GLU	N	152	-36.27	-36.27	12.07
GLU	CA	152	-36.43	-24.83	12.73	:	GLU	CB	152	-37.92	-37.92	13.18

FIG. 1.11.

GLU	CG	152	-38.53	-25.06	14.54	:	GLU	CD	152	-38.34	-38.34	15.68
GLU	OE1	152	-38.86	-24.28	16.80	:	GLU	OE2	152	-37.74	-37.74	15.41
GLU	C	152	-35.43	-24.88	13.88	:	GLU	O	152	-35.53	-35.53	14.96
ALA	N	153	-34.29	-24.55	13.27	:	ALA	CA	153	-32.93	-32.93	13.81
ALA	CB	153	-32.52	-25.77	14.62	:	ALA	C	153	-32.18	-32.18	12.52
ALA	O	153	-31.36	-23.84	12.22	:	GLN	N	154	-32.53	-32.53	11.68
GLN	CA	154	-31.77	-25.92	10.51	:	GLN	CB	154	-30.63	-30.63	11.02
GLN	CG	154	-30.97	-28.24	11.41	:	GLN	CD	154	-31.29	-31.29	10.12
GLN	OE1	154	-32.46	-29.28	9.86	:	GLN	NE2	154	-30.33	-30.33	9.20
GLN	C	154	-32.29	-26.35	9.15	:	GLN	O	154	-31.39	-31.39	8.34
GLN	N	155	-33.50	-26.68	8.69	:	GLN	CA	155	-33.76	-33.76	7.22
GLN	CB	155	-33.41	-25.57	6.45	:	GLN	CG	155	-33.48	-33.48	4.93
GLN	CD	155	-34.59	-24.56	4.35	:	GLN	OE1	155	-35.54	-35.54	5.03
GLN	NE2	155	-34.53	-24.23	3.04	:	GLN	C	155	-33.11	-33.11	6.47
GLN	O	155	-31.92	-28.10	6.31	:	SER	N	156	-33.85	-33.85	5.98
SER	CA	156	-33.32	-30.25	5.33	:	SER	CB	156	-34.46	-34.46	4.97
SER	OG	156	-34.05	-32.24	4.10	:	SER	C	156	-32.58	-32.58	4.06
SER	O	156	-33.19	-29.19	3.24	:	TYR	N	157	-31.37	-31.37	3.75
TYR	CA	157	-30.76	-30.07	2.49	:	TYR	CB	157	-29.40	-29.40	2.33
TYR	CG	157	-29.27	-32.19	2.37	:	TYR	CD1	157	-28.82	-28.82	3.49
TYR	CE1	157	-28.72	-34.17	3.53	:	TYR	CD2	157	-29.61	-29.61	1.27
TYR	CE2	157	-29.51	-34.25	1.30	:	TYR	CZ	157	-29.07	-29.07	2.42
TYR	OH	157	-29.03	-36.25	2.43	:	TYR	C	157	-31.63	-31.63	1.30
TYR	O	157	-31.46	-29.87	0.24	:	LEU	N	158	-32.64	-32.64	1.42
LEU	CA	158	-33.60	-31.62	0.34	:	LEU	CB	158	-34.71	-34.71	0.75
LEU	CG	158	-34.74	-34.06	0.44	:	LEU	CD1	158	-33.92	-33.92	-0.79
LEU	CD2	158	-34.18	-34.87	1.58	:	LEU	C	158	-34.32	-34.32	-0.11
LEU	O	158	-34.67	-30.20	-1.28	:	GLN	N	159	-34.53	-34.53	0.79
GLN	CA	159	-35.19	-28.14	0.45	:	GLN	CB	159	-35.47	-35.47	1.68
GLN	CG	159	-36.42	-28.08	2.55	:	GLN	CD	159	-36.61	-36.61	3.91
GLN	OE1	159	-36.07	-27.90	4.93	:	GLN	NE2	159	-37.44	-37.44	3.94
GLN	C	159	-34.41	-27.27	-0.51	:	GLN	O	159	-35.04	-35.04	-0.99
GLU	N	160	-33.14	-27.46	-0.84	:	GLU	CA	160	-32.50	-32.50	-1.76
GLU	CB	160	-31.04	-26.48	-1.45	:	GLU	CG	160	-30.73	-30.73	-0.11
GLU	CD	160	-31.52	-24.58	0.25	:	GLU	OE1	160	-32.00	-32.00	1.40
GLU	OE2	160	-31.65	-23.66	-0.59	:	GLU	C	160	-32.67	-32.67	-3.23
GLU	O	160	-32.28	-26.13	-4.15	:	PHE	N	161	-33.23	-33.23	-3.47
PHE	CA	161	-33.52	-28.52	-4.81	:	PHE	CB	161	-33.79	-33.79	-4.78
PHE	CG	161	-32.49	-30.74	-4.67	:	PHE	CD1	161	-32.25	-32.25	-3.56
PHE	CD2	161	-31.58	-30.60	-5.67	:	PHE	CE1	161	-31.05	-31.05	-3.45
PHE	CE2	161	-30.39	-31.25	-5.56	:	PHE	CZ	161	-30.14	-30.14	-4.45
PHE	C	161	-34.73	-27.77	-5.30	:	PHE	O	161	-35.53	-35.53	-4.50
SER	N	162	-34.89	-27.59	-6.60	:	SER	CA	162	-35.97	-35.97	-7.03
SER	CB	162	-35.61	-26.30	-8.44	:	SER	OG	162	-35.27	-35.27	-9.16
SER	C	162	-37.31	-27.46	-6.94	:	SER	O	162	-37.35	-37.35	-6.63
LYS	N	163	-38.45	-26.84	-7.21	:	LYS	CA	163	-39.72	-39.72	-6.99
LYS	CB	163	-40.84	-26.56	-7.22	:	LYS	CG	163	-41.94	-41.94	-6.24
LYS	CD	163	-43.08	-25.68	-6.74	:	LYS	CE	163	-43.78	-43.78	-8.06
LYS	NZ	163	-44.10	-27.66	-8.04	:	LYS	C	163	-39.90	-39.90	-7.95
LYS	O	163	-40.17	-29.76	-7.52	:	HIS	N	164	-39.73	-39.73	-9.25
HIS	CA	164	-39.92	-29.49	-10.23	:	HIS	CB	164	-39.64	-39.64	-11.68
HIS	CG	164	-39.24	-30.07	-12.73	:	HIS	CD2	164	-39.59	-39.59	-14.10
HIS	ND1	164	-38.45	-31.19	-12.61	:	HIS	CE1	164	-38.32	-38.32	-13.78
HIS	NE2	164	-39.01	-31.07	-14.68	:	HIS	C	164	-38.99	-38.99	-9.92
HIS	O	164	-39.39	-31.79	-10.14	:	ILE	N	165	-37.72	-37.72	-9.55
ILE	CA	165	-36.87	-31.57	-9.33	:	ILE	CB	165	-35.45	-35.45	-9.14
ILE	CG2	165	-34.53	-31.98	-8.41	:	ILE	CG1	165	-35.02	-35.02	-10.55
ILE	CD1	165	-33.58	-30.40	-10.81	:	ILE	C	165	-37.40	-37.40	-8.15
ILE	O	165	-37.41	-33.62	-8.28	:	LEU	N	166	-37.98	-37.98	-7.11

FIG. 1·12.

LEU	CA	166	-38.48	-32.52	-5.97	:	LEU	CB	166	-38.75	-38.75	-4.84
LEU	CG	166	-37.87	-31.47	-3.61	:	LEU	CD1	166	-36.66	-36.66	-3.74
LEU	CD2	166	-37.41	-30.07	-3.44	:	LEU	C	166	-39.74	-39.74	-6.38
LEU	O	166	-39.85	-34.47	-6.15	:	GLU	N	167	-40.65	-40.65	-7.09
GLU	CA	167	-41.88	-33.22	-7.51	:	GLU	CB	167	-42.78	-42.78	-8.24
GLU	CG	167	-43.37	-31.11	-7.44	:	GLU	CD	167	-44.52	-44.52	-8.19
GLU	OE1	167	-44.47	-30.18	-9.38	:	GLU	OE2	167	-45.55	-45.55	-7.60
GLU	C	167	-41.59	-34.41	-8.44	:	GLU	O	167	-42.08	-42.08	-8.22
ALA	N	168	-40.67	-34.28	-9.38	:	ALA	CA	168	-40.46	-40.46	-10.34
ALA	CB	168	-39.68	-34.79	-11.48	:	ALA	C	168	-39.72	-39.72	-9.65
ALA	O	168	-40.04	-37.62	-9.85	:	SER	N	169	-38.77	-38.77	-8.78
SER	CA	169	-38.10	-37.14	-7.99	:	SER	CB	169	-37.07	-37.07	-7.08
SER	OG	169	-36.02	-35.94	-7.82	:	SER	C	169	-39.05	-39.05	-7.11
SER	O	169	-39.19	-39.13	-7.32	:	PHE	N	170	-39.72	-39.72	-6.14
PHE	CA	170	-40.60	-38.05	-5.25	:	PHE	CB	170	-40.81	-40.81	-3.95
PHE	CG	170	-39.54	-37.04	-3.13	:	PHE	CD1	170	-38.85	-38.85	-2.68
PHE	CD2	170	-39.05	-35.79	-2.91	:	PHE	CE1	170	-37.67	-37.67	-2.01
PHE	CE2	170	-37.86	-35.62	-2.24	:	PHE	CZ	170	-37.17	-37.17	-1.80
PHE	C	170	-41.93	-38.40	-5.87	:	PHE	O	170	-42.70	-42.70	-5.20
ASN	N	171	-42.20	-37.98	-7.15	:	ASN	CA	171	-43.44	-43.44	-7.90
ASN	CB	171	-43.57	-39.73	-8.24	:	ASN	CG	171	-44.74	-44.74	-9.18
ASN	OD1	171	-45.26	-39.16	-9.87	:	ASN	ND2	171	-45.21	-45.21	-9.32
ASN	C	171	-44.62	-37.83	-7.04	:	ASN	O	171	-45.26	-45.26	-6.40
SER	N	172	-44.83	-36.55	-6.83	:	SER	CA	172	-45.90	-45.90	-5.98
SER	CB	172	-45.57	-36.23	-4.50	:	SER	OG	172	-45.71	-45.71	-3.99
SER	C	172	-46.11	-34.56	-6.24	:	SER	O	172	-45.29	-45.29	-6.91
LYS	N	173	-47.28	-34.04	-5.85	:	LYS	CA	173	-47.49	-47.49	-6.01
LYS	CB	173	-48.99	-32.46	-6.05	:	LYS	CG	173	-49.45	-49.45	-7.51
LYS	CD	173	-48.84	-31.14	-8.27	:	LYS	CE	173	-48.12	-48.12	-9.70
LYS	NZ	173	-46.79	-32.04	-9.69	:	LYS	C	173	-46.74	-46.74	-4.89
LYS	O	173	-46.52	-32.54	-3.83	:	PHE	N	174	-46.22	-46.22	-5.17
PHE	CA	174	-45.24	-30.19	-4.25	:	PHE	CB	174	-44.62	-44.62	-4.82
PHE	CG	174	-43.66	-28.22	-3.79	:	PHE	CD1	174	-42.48	-42.48	-3.41
PHE	CD2	174	-44.03	-27.09	-3.08	:	PHE	CE1	174	-41.73	-41.73	-2.34
PHE	CE2	174	-43.29	-26.63	-2.02	:	PHE	CZ	174	-42.14	-42.14	-1.65
PHE	C	174	-45.80	-29.98	-2.84	:	PHE	O	174	-45.15	-45.15	-1.85
GLU	N	175	-46.96	-29.41	-2.74	:	GLU	CA	175	-47.58	-47.58	-1.48
GLU	CB	175	-48.89	-28.45	-1.62	:	GLU	CG	175	-50.07	-50.07	-2.47
GLU	CD	175	-49.50	-29.57	-3.75	:	GLU	OE1	175	-49.33	-49.33	-3.67
GLU	OE2	175	-49.07	-28.86	-4.71	:	GLU	C	175	-47.78	-47.78	-0.88
GLU	O	175	-47.70	-30.65	0.34	:	GLU	N	176	-47.91	-47.91	-1.48
GLU	CA	176	-47.95	-33.04	-0.68	:	GLU	CB	176	-48.39	-48.39	-1.56
GLU	CG	176	-48.15	-35.69	-1.26	:	GLU	CD	176	-48.70	-48.70	0.07
GLU	OE1	176	-49.05	-35.53	1.02	:	GLU	OE2	176	-48.73	-48.73	0.14
GLU	C	176	-46.56	-33.27	-0.05	:	GLU	O	176	-46.47	-46.47	1.19
ILE	N	177	-45.47	-33.25	-0.86	:	ILE	CA	177	-44.04	-44.04	-0.46
ILE	CB	177	-43.04	-33.02	-1.60	:	ILE	CG2	177	-41.64	-41.64	-1.10
ILE	CG1	177	-42.95	-34.20	-2.52	:	ILE	CD1	177	-42.17	-42.17	-3.84
ILE	C	177	-43.76	-32.42	0.67	:	ILE	O	177	-43.05	-43.05	1.61
ASN	N	178	-44.28	-31.22	0.68	:	ASN	CA	178	-43.94	-43.94	1.71
ASN	CB	178	-44.32	-28.95	1.15	:	ASN	CG	178	-43.69	-43.69	1.96
ASN	OD1	178	-43.06	-26.95	1.36	:	ASN	ND2	178	-43.77	-43.77	3.30
ASN	C	178	-44.63	-30.59	3.07	:	ASN	O	178	-44.02	-44.02	4.14
ARG	N	179	-45.93	-30.90	3.05	:	ARG	CA	179	-46.74	-46.74	4.23
ARG	CB	179	-48.20	-31.51	3.86	:	ARG	CG	179	-49.14	-49.14	4.89
ARG	CD	179	-50.28	-32.84	4.05	:	ARG	NE	179	-50.02	-50.02	3.53
ARG	CZ	179	-49.94	-35.31	4.35	:	ARG	NH1	179	-49.70	-49.70	3.82
ARG	NH2	179	-50.05	-35.12	5.70	:	ARG	C	179	-46.15	-46.15	4.82
ARG	O	179	-45.87	-32.43	6.01	:	VAL	N	180	-45.89	-45.89	4.03

FIG. 1.13.

VAL	CA	180	-45.38	-34.66	4.73	:	VAL	CB	180	-45.76	-45.76	3.89
VAL	CG1	180	-45.60	-35.78	2.39	:	VAL	CG2	180	-44.82	-44.82	4.29
VAL	C	180	-43.89	-34.57	5.13	:	VAL	O	180	-43.55	-43.55	6.21
LEU	N	181	-42.99	-33.92	4.36	:	LEU	CA	181	-41.53	-41.53	4.64
LEU	CB	181	-40.79	-33.84	3.34	:	LEU	CG	181	-39.78	-39.78	3.09
LEU	CD1	181	-40.23	-36.27	3.52	:	LEU	CD2	181	-39.50	-39.50	1.60
LEU	C	181	-40.99	-32.51	5.36	:	LEU	O	181	-40.01	-40.01	6.08
PHE	N	182	-41.55	-31.34	5.15	:	PHE	CA	182	-40.95	-40.95	5.61
PHE	CB	182	-40.31	-29.33	4.46	:	PHE	CG	182	-39.44	-39.44	3.49
PHE	CD1	182	-38.40	-30.89	3.94	:	PHE	CD2	182	-39.73	-39.73	2.15
PHE	CE1	182	-37.66	-31.60	3.04	:	PHE	CE2	182	-38.98	-38.98	1.26
PHE	CZ	182	-37.95	-31.53	1.70	:	PHE	C	182	-41.98	-41.98	6.23
PHE	O	182	-41.68	-27.96	6.39	:	GLU	N	183	-43.21	-43.21	6.58
GLU	CA	183	-44.16	-28.56	7.08	:	GLU	CB	183	-45.55	-45.55	7.01
GLU	CG	183	-46.88	-28.39	7.04	:	GLU	CD	183	-48.14	-48.14	7.08
GLU	OE1	183	-48.11	-30.36	7.91	:	GLU	OE2	183	-49.13	-49.13	6.28
GLU	C	183	-43.73	-28.16	8.52	:	GLU	O	183	-43.31	-43.31	9.40
GLU	N	184	-43.76	-26.81	8.57	:	GLU	CA	184	-43.26	-43.26	9.65
GLU	CB	184	-43.51	-24.46	9.22	:	GLU	CG	184	-42.95	-42.95	10.10
GLU	CD	184	-44.00	-22.66	11.05	:	GLU	OE1	184	-44.07	-44.07	11.05
GLU	OE2	184	-44.76	-23.39	11.77	:	GLU	C	184	-43.79	-43.79	11.02
GLU	O	184	-42.96	-26.41	11.92	:	GLU	N	185	-45.08	-45.08	11.30
GLU	CA	185	-45.43	-26.70	12.65	:	GLU	CB	185	-46.90	-46.90	13.08
GLU	CG	185	-46.99	-26.66	14.64	:	GLU	CD	185	-45.94	-45.94	15.47
GLU	OE1	185	-44.76	-26.28	15.58	:	GLU	OE2	185	-46.35	-46.35	16.00
GLU	C	185	-45.25	-28.21	12.60	:	GLU	O	185	-45.30	-45.30	11.50
GLY	N	186	-45.01	-28.94	13.67	:	GLY	CA	186	-44.73	-44.73	13.46
GLY	C	186	-43.27	-30.58	13.06	:	GLY	O	186	-42.78	-42.78	13.16
GLN	N	187	-42.57	-29.50	12.62	:	GLN	CA	187	-41.12	-41.12	12.52
GLN	CB	187	-40.50	-28.24	12.16	:	GLN	CG	187	-40.31	-40.31	10.69
GLN	CD	187	-39.52	-26.85	10.63	:	GLN	OE1	187	-38.30	-38.30	10.37
GLN	NE2	187	-40.12	-25.69	10.96	:	GLN	C	187	-40.64	-40.64	13.93
GLN	O	187	-41.39	-29.59	14.91	:	GLN	N	188	-39.35	-39.35	14.08
GLN	CA	188	-38.95	-30.45	15.36	:	GLN	CB	188	-38.47	-38.47	14.97
GLN	CG	188	-37.95	-32.96	15.92	:	GLN	CD	188	-38.88	-38.88	17.09
GLN	OE1	188	-39.62	-34.07	17.25	:	GLN	NE2	188	-38.86	-38.86	18.00
GLN	C	188	-37.99	-29.54	16.09	:	GLN	O	188	-37.27	-37.27	16.85
GLU	N	189	-37.78	-28.23	16.04	:	GLU	CA	189	-36.82	-36.82	16.92
GLU	CB	189	-37.18	-27.67	18.44	:	GLU	CG	189	-38.04	-38.04	18.86
GLU	CD	189	-38.38	-26.37	20.37	:	GLU	OE1	189	-39.57	-39.57	20.73
GLU	OE2	189	-37.47	-25.97	21.18	:	GLU	C	189	-35.32	-35.32	16.84
GLU	O	189	-34.54	-27.00	17.38	:	GLY	N	190	-34.76	-34.76	16.25
GLY	CA	190	-33.31	-28.93	16.30	:	GLY	C	190	-32.80	-32.80	16.19
GLY	O	190	-33.56	-31.26	16.36	:	VAL	N	191	-31.52	-31.52	15.94
VAL	CA	191	-30.98	-31.72	15.64	:	VAL	CB	191	-29.79	-29.79	14.73
VAL	CG1	191	-30.23	-30.73	13.55	:	VAL	CG2	191	-28.70	-28.70	15.34
VAL	C	191	-30.61	-32.61	16.79	:	VAL	O	191	-30.10	-30.10	16.51
ILE	N	192	-30.73	-32.32	18.08	:	ILE	CA	192	-30.34	-30.34	19.14
ILE	CB	192	-29.21	-32.72	20.03	:	ILE	CG2	192	-29.09	-29.09	21.14
ILE	CG1	192	-27.85	-32.61	19.35	:	ILE	CD1	192	-26.85	-26.85	20.05
ILE	C	192	-31.65	-33.12	19.86	:	ILE	O	192	-31.93	-31.93	20.50
VAL	N	193	-32.49	-34.08	19.52	:	VAL	CA	193	-33.88	-33.88	19.95
VAL	CB	193	-34.67	-34.82	18.79	:	VAL	CG1	193	-35.79	-35.79	19.25
VAL	CG2	193	-35.32	-33.72	18.02	:	VAL	C	193	-33.82	-33.82	21.13
VAL	O	193	-33.00	-36.07	21.05	:	ASN	N	194	-34.61	-34.61	22.19
ASN	CA	194	-34.53	-36.17	23.13	:	ASN	CB	194	-34.64	-34.64	24.57
ASN	CG	194	-35.99	-35.21	24.89	:	ASN	OD1	194	-36.50	-36.50	24.14
ASN	ND2	194	-36.52	-35.72	26.01	:	ASN	C	194	-35.74	-35.74	22.82
ASN	O	194	-36.82	-36.56	22.44	:	ILE	N	195	-35.47	-35.47	22.91

FIG. 1.14.

ILE	CA	195	-36.53	-39.25	22.68	:	ILE	CB	195	-36.12	-36.12	21.69
ILE	CG2	195	-36.41	-39.57	20.41	:	ILE	CG1	195	-34.73	-34.73	21.79
ILE	CD1	195	-34.46	-41.71	23.06	:	ILE	C	195	-36.83	-36.83	24.03
ILE	O	195	-36.34	-39.35	25.07	:	ASP	N	196	-37.63	-37.63	24.03
ASP	CA	196	-37.98	-41.53	25.27	:	ASP	CB	196	-39.52	-39.52	25.40
ASP	CG	196	-40.08	-42.81	25.97	:	ASP	OD1	196	-40.21	-40.21	27.21
ASP	OD2	196	-40.21	-43.76	25.15	:	ASP	C	196	-37.43	-37.43	25.38
ASP	O	196	-37.40	-43.83	24.50	:	SER	N	197	-37.22	-37.22	26.67
SER	CA	197	-36.86	-44.22	27.41	:	SER	CB	197	-37.51	-37.51	28.78
SER	OG	197	-37.60	-42.68	29.18	:	SER	C	197	-37.28	-37.28	26.73
SER	O	197	-36.40	-46.33	26.38	:	GLU	N	198	-38.60	-38.60	26.48
GLU	CA	198	-39.08	-46.78	25.81	:	GLU	CB	198	-40.60	-40.60	25.64
GLU	CG	198	-41.35	-46.78	27.01	:	GLU	CD	198	-42.11	-42.11	27.37
GLU	OE1	198	-41.91	-44.98	28.52	:	GLU	OE2	198	-42.90	-42.90	26.48
GLU	C	198	-38.45	-47.06	24.42	:	GLU	O	198	-37.90	-37.90	24.27
GLN	N	199	-38.43	-46.12	23.43	:	GLN	CA	199	-37.81	-37.81	22.13
GLN	CB	199	-37.74	-45.11	21.28	:	GLN	CG	199	-39.11	-39.11	20.94
GLN	CD	199	-39.18	-42.89	20.83	:	GLN	OE1	199	-38.88	-38.88	21.83
GLN	NE2	199	-39.59	-42.26	19.71	:	GLN	C	199	-36.38	-36.38	22.25
GLN	O	199	-36.07	-48.15	21.75	:	ILE	N	200	-35.52	-35.52	23.06
ILE	CA	200	-34.13	-46.81	23.22	:	ILE	CB	200	-33.47	-33.47	24.42
ILE	CG2	200	-31.99	-46.51	24.49	:	ILE	CG1	200	-33.68	-33.68	24.33
ILE	CD1	200	-33.59	-43.99	25.72	:	ILE	C	200	-33.96	-33.96	23.44
ILE	O	200	-33.10	-48.96	22.80	:	LYS	N	201	-34.83	-34.83	24.34
LYS	CA	201	-34.70	-50.22	24.82	:	LYS	CB	201	-35.92	-35.92	25.67
LYS	CG	201	-35.62	-52.09	26.34	:	LYS	CD	201	-36.83	-36.83	27.05
LYS	CE	201	-36.35	-53.82	28.11	:	LYS	NZ	201	-37.41	-37.41	29.00
LYS	C	201	-34.53	-51.28	23.74	:	LYS	O	201	-33.53	-33.53	23.78
GLU	N	202	-35.49	-51.25	22.78	:	GLU	CA	202	-35.47	-35.47	21.89
GLU	CB	202	-36.76	-52.38	21.01	:	GLU	CG	202	-37.04	-37.04	20.13
GLU	CD	202	-36.64	-55.03	20.75	:	GLU	OE1	202	-35.44	-35.44	20.69
GLU	OE2	202	-37.47	-55.63	21.48	:	GLU	C	202	-34.15	-34.15	21.09
GLU	O	202	-33.33	-53.26	21.13	:	LEU	N	203	-33.88	-33.88	20.68
LEU	CA	203	-32.64	-50.63	19.98	:	LEU	CB	203	-32.68	-32.68	19.63
LEU	CG	203	-31.99	-48.42	18.48	:	LEU	CD1	203	-31.37	-31.37	19.00
LEU	CD2	203	-30.92	-49.27	17.86	:	LEU	C	203	-31.39	-31.39	20.84
LEU	O	203	-30.42	-51.45	20.23	:	SER	N	204	-31.33	-31.33	22.20
SER	CA	204	-30.06	-50.93	22.91	:	SER	CB	204	-30.09	-30.09	24.36
SER	OG	204	-30.72	-49.47	24.62	:	SER	C	204	-29.61	-29.61	22.83
SER	O	204	-28.43	-52.69	22.61	:	LYS	N	205	-30.67	-30.67	23.01
LYS	CA	205	-30.57	-54.59	23.03	:	LYS	CB	205	-31.98	-31.98	23.07
LYS	CG	205	-32.16	-56.55	23.41	:	LYS	CD	205	-33.66	-33.66	23.17
LYS	CE	205	-34.57	-55.86	24.09	:	LYS	NZ	205	-35.57	-35.57	23.29
LYS	C	205	-29.80	-55.13	21.83	:	LYS	O	205	-28.68	-28.68	21.92
HIS	N	206	-30.44	-54.82	20.69	:	HIS	CA	206	-29.90	-29.90	19.40
HIS	CB	206	-30.87	-54.72	18.31	:	HIS	CG	206	-30.37	-30.37	16.97
HIS	CD2	206	-30.02	-56.52	16.69	:	HIS	ND1	206	-30.07	-30.07	15.89
HIS	CE1	206	-29.55	-55.30	14.97	:	HIS	NE2	206	-29.52	-29.52	15.47
HIS	C	206	-28.46	-54.70	19.19	:	HIS	O	206	-27.62	-27.62	18.82
ALA	N	207	-28.16	-53.42	19.47	:	ALA	CA	207	-26.81	-26.81	19.35
ALA	CB	207	-26.83	-51.46	19.86	:	ALA	C	207	-25.76	-25.76	20.12
ALA	O	207	-24.74	-54.22	19.60	:	LYS	N	208	-26.10	-26.10	21.40
LYS	CA	208	-25.19	-54.66	22.33	:	LYS	CB	208	-25.85	-25.85	23.68
LYS	CG	208	-25.67	-53.54	24.54	:	LYS	CD	208	-26.66	-26.66	25.65
LYS	CE	208	-26.62	-52.92	26.82	:	LYS	NZ	208	-25.33	-25.33	27.46
LYS	C	208	-24.74	-56.04	21.89	:	LYS	O	208	-23.58	-23.58	22.03
SER	N	209	-25.75	-56.67	21.30	:	SER	CA	209	-25.56	-25.56	20.74
SER	CB	209	-26.86	-58.46	20.24	:	SER	OG	209	-27.49	-27.49	21.51
SER	C	209	-24.55	-57.92	19.65	:	SER	O	209	-23.57	-23.57	19.72

FIG. 1.15.

SER	N	210	-24.84	-56.91	18.81	:	SER	CA	210	-24.14	-24.14	17.55
SER	CB	210	-24.79	-55.56	16.74	:	SER	OG	210	-26.24	-26.24	16.62
SER	C	210	-22.69	-56.40	17.84	:	SER	O	210	-21.85	-21.85	17.14
SER	N	211	-22.43	-55.62	18.90	:	SER	CA	211	-21.06	-21.06	19.26
SER	CB	211	-21.18	-53.82	19.82	:	SER	OG	211	-22.03	-22.03	19.04
SER	C	211	-20.55	-56.28	20.30	:	SER	O	211	-21.06	-21.06	20.27
ARG	N	212	-19.64	-55.88	21.24	:	ARG	CA	212	-19.04	-19.04	22.40
ARG	CB	212	-19.73	-57.98	22.87	:	ARG	CG	212	-21.16	-21.16	23.41
ARG	CD	212	-21.77	-59.17	22.72	:	ARG	NE	212	-23.25	-23.25	22.62
ARG	CZ	212	-24.10	-59.38	23.70	:	ARG	NH1	212	-25.47	-25.47	23.54
ARG	NH2	212	-23.53	-59.40	24.98	:	ARG	C	212	-17.62	-17.62	22.00
ARG	OT1	212	-16.65	-56.67	22.70	:	ARG	OT2	212	-17.56	-17.56	21.00
ASN	CB	220	-3.63	-53.54	26.53	:	ASN	CG	220	-4.61	-4.61	27.75
ASN	OD1	220	-5.39	-52.66	28.00	:	ASN	ND2	220	-4.60	-4.60	28.56
ASN	C	220	-2.45	-51.28	26.97	:	ASN	O	220	-1.34	-1.34	26.60
ASN	N	220	-2.82	-52.06	24.65	:	ASN	CA	220	-3.41	-3.41	25.99
THR	N	221	-2.92	-51.16	28.19	:	THR	CA	221	-2.36	-2.36	29.22
THR	CB	221	-3.37	-50.58	30.35	:	THR	OG1	221	-4.72	-4.72	29.83
THR	CG2	221	-3.28	-49.38	31.32	:	THR	C	221	-0.90	-0.90	29.67
THR	O	221	-0.28	-51.48	29.55	:	ILE	N	222	-0.28	-0.28	30.16
ILE	CA	222	1.02	-49.41	30.76	:	ILE	CB	222	2.12	2.12	29.77
ILE	CG2	222	2.01	-47.64	29.26	:	ILE	CG1	222	3.44	3.44	30.50
ILE	CD1	222	4.70	-48.79	29.65	:	ILE	C	222	0.98	0.98	31.85
ILE	O	222	0.40	-47.29	31.64	:	GLY	N	223	1.49	1.49	33.04
GLY	CA	223	1.38	-47.40	34.00	:	GLY	C	223	1.18	1.18	35.40
GLY	O	223	0.89	-49.16	35.54	:	ASN	N	224	1.23	1.23	36.42
ASN	CA	224	1.45	-47.62	37.75	:	ASN	CB	224	2.90	2.90	38.00
ASN	CG	224	3.38	-45.94	38.17	:	ASN	OD1	224	2.60	2.60	38.26
ASN	ND2	224	4.71	-45.80	38.28	:	ASN	C	224	0.57	0.57	38.76
ASN	O	224	-0.55	-46.64	38.42	:	GLU	N	225	1.00	1.00	39.97
GLU	CA	225	0.17	-46.01	40.98	:	GLU	CB	225	0.87	0.87	42.36
GLU	CG	225	1.73	-47.04	42.87	:	GLU	CD	225	3.18	3.18	42.26
GLU	OE1	225	3.37	-47.69	41.13	:	GLU	OE2	225	4.11	4.11	42.99
GLU	C	225	-0.24	-44.56	40.63	:	GLU	O	225	-1.27	-1.27	41.14
PHE	N	226	0.53	-43.83	39.81	:	PHE	CA	226	0.27	0.27	39.57
PHE	CB	226	1.49	-41.64	39.60	:	PHE	CG	226	2.30	2.30	40.80
PHE	CD1	226	3.13	-42.94	40.85	:	PHE	CD2	226	2.20	2.20	41.81
PHE	CE1	226	3.90	-43.11	41.96	:	PHE	CE2	226	2.97	2.97	42.92
PHE	CZ	226	3.83	-42.21	42.99	:	PHE	C	226	-0.38	-0.38	38.26
PHE	O	226	-0.82	-40.89	38.08	:	GLY	N	227	-0.27	-0.27	37.26
GLY	CA	227	-0.95	-42.66	36.02	:	GLY	C	227	-0.88	-0.88	35.17
GLY	O	227	-0.09	-44.77	35.49	:	ASN	N	228	-1.66	-1.66	34.14
ASN	CA	228	-1.38	-45.14	33.23	:	ASN	CB	228	-1.77	-1.77	33.78
ASN	CG	228	-3.14	-46.74	34.35	:	ASN	OD1	228	-4.14	-4.14	33.82
ASN	ND2	228	-3.17	-47.51	35.44	:	ASN	C	228	-2.10	-2.10	31.97
ASN	O	228	-2.97	-43.95	31.93	:	LEU	N	229	-1.38	-1.38	30.96
LEU	CA	229	-1.54	-44.92	29.56	:	LEU	CB	229	-0.13	-0.13	29.09
LEU	CG	229	0.32	-43.99	27.78	:	LEU	CD1	229	1.82	1.82	27.80
LEU	CD2	229	-0.01	-44.89	26.65	:	LEU	C	229	-2.10	-2.10	28.78
LEU	O	229	-1.41	-47.11	28.73	:	THR	N	230	-3.25	-3.25	28.11
THR	CA	230	-3.60	-47.21	27.31	:	THR	CB	230	-4.69	-4.69	28.12
THR	OG1	230	-4.96	-49.13	27.32	:	THR	CG2	230	-5.95	-5.95	28.42
THR	C	230	-3.99	-46.79	25.88	:	THR	O	230	-5.11	-5.11	25.53
GLU	N	231	-2.86	-46.84	25.15	:	GLU	CA	231	-2.62	-2.62	23.70
GLU	CB	231	-1.12	-46.64	23.50	:	GLU	CG	231	-0.49	-0.49	22.53
GLU	CD	231	0.30	-44.52	23.16	:	GLU	OE1	231	1.49	1.49	23.33
GLU	OE2	231	-0.18	-43.40	23.45	:	GLU	C	231	-3.21	-3.21	22.85
GLU	O	231	-3.09	-48.90	23.28	:	ARG	N	232	-3.78	-3.78	21.67
ARG	CA	232	-4.30	-48.65	20.79	:	ARG	CB	232	-5.79	-5.79	21.15

FIG. 1.16

ARG	CG	232	-6.85	-47.96	21.46	:	ARG	CD	232	-8.00	-8.00	22.47
ARG	NE	232	-8.92	-47.23	22.81	:	ARG	CZ	232	-8.52	-8.52	23.58
ARG	NH1	232	-9.35	-45.17	23.79	:	ARG	NH2	232	-7.35	-7.35	24.27
ARG	C	232	-4.25	-48.12	19.35	:	ARG	O	232	-4.69	-4.69	19.19
THR	N	233	-3.73	-48.78	18.28	:	THR	CA	233	-3.62	-3.62	17.01
THR	CB	233	-2.17	-48.08	16.41	:	THR	OG1	233	-2.13	-2.13	15.30
THR	CG2	233	-1.14	-48.51	17.43	:	THR	C	233	-4.57	-4.57	15.98
THR	O	233	-4.88	-49.78	16.03	:	ASP	N	234	-4.97	-4.97	15.02
ASP	CA	234	-5.81	-48.29	13.94	:	ASP	CB	234	-6.97	-6.97	13.64
ASP	CG	234	-7.66	-47.55	12.30	:	ASP	OD1	234	-8.86	-8.86	12.27
ASP	OD2	234	-7.07	-47.39	11.23	:	ASP	C	234	-4.84	-4.84	12.80
ASP	O	234	-4.30	-47.12	12.60	:	ASN	N	235	-4.57	-4.57	11.96
ASN	CA	235	-3.64	-48.91	10.92	:	ASN	CB	235	-2.35	-2.35	10.86
ASN	CG	235	-1.49	-49.33	9.62	:	ASN	OD1	235	-1.82	-1.82	8.80
ASN	ND2	235	-0.31	-49.97	9.47	:	ASN	C	235	-4.43	-4.43	9.66
ASN	O	235	-4.34	-50.11	8.98	:	SER	N	236	-5.24	-5.24	9.39
SER	CA	236	-6.03	-48.05	8.17	:	SER	CB	236	-7.12	-7.12	8.20
SER	OG	236	-8.00	-49.08	9.35	:	SER	C	236	-6.64	-6.64	8.36
SER	O	236	-7.88	-46.40	8.30	:	LEU	N	237	-5.68	-5.68	8.74
LEU	CA	237	-5.86	-44.50	9.29	:	LEU	CB	237	-6.75	-6.75	10.48
LEU	CG	237	-8.19	-44.14	10.16	:	LEU	CD1	237	-8.96	-8.96	11.40
LEU	CD2	237	-8.38	-42.70	9.69	:	LEU	C	237	-4.47	-4.47	9.82
LEU	O	237	-3.94	-43.17	9.64	:	ASN	N	238	-3.86	-3.86	10.46
ASN	CA	238	-2.50	-45.17	10.93	:	ASN	CB	238	-1.67	-1.67	9.68
ASN	CG	238	-0.31	-44.40	9.89	:	ASN	OD1	238	0.29	0.29	9.03
ASN	ND2	238	0.35	-44.56	11.03	:	ASN	C	238	-2.52	-2.52	11.91
ASN	O	238	-1.76	-43.01	11.87	:	VAL	N	239	-3.45	-3.45	12.86
VAL	CA	239	-3.76	-43.13	13.90	:	VAL	CB	239	-5.19	-5.19	13.68
VAL	CG1	239	-5.83	-41.98	14.85	:	VAL	CG2	239	-5.14	-5.14	12.56
VAL	C	239	-3.58	-43.91	15.20	:	VAL	O	239	-3.80	-3.80	15.23
LEU	N	240	-3.19	-43.34	16.32	:	LEU	CA	240	-3.07	-3.07	17.60
LEU	CB	240	-1.75	-43.57	18.07	:	LEU	CG	240	-0.83	-0.83	19.08
LEU	CD1	240	0.36	-44.71	18.37	:	LEU	CD2	240	-0.27	-0.27	19.91
LEU	C	240	-4.27	-43.54	18.44	:	LEU	O	240	-4.50	-4.50	18.32
ILE	N	241	-5.13	-44.19	19.24	:	ILE	CA	241	-6.14	-6.14	20.02
ILE	CB	241	-7.53	-44.12	19.92	:	ILE	CG2	241	-8.50	-8.50	20.76
ILE	CG1	241	-8.03	-44.07	18.52	:	ILE	CD1	241	-9.07	-9.07	18.39
ILE	C	241	-5.61	-43.75	21.41	:	ILE	O	241	-5.86	-5.86	22.00
SER	N	242	-4.84	-42.83	21.96	:	SER	CA	242	-4.23	-4.23	23.26
SER	CB	242	-2.89	-42.33	23.24	:	SER	OG	242	-2.74	-2.74	23.89
SER	C	242	-5.18	-42.50	24.33	:	SER	O	242	-6.08	-6.08	24.03
SER	N	243	-4.98	-42.78	25.60	:	SER	CA	243	-5.95	-5.95	26.62
SER	CB	243	-6.88	-43.62	26.47	:	SER	OG	243	-7.79	-7.79	27.53
SER	C	243	-5.10	-42.48	27.86	:	SER	O	243	-4.61	-4.61	28.18
ILE	N	244	-4.89	-41.37	28.56	:	ILE	CA	244	-3.88	-3.88	29.62
ILE	CB	244	-2.91	-40.11	29.23	:	ILE	CG2	244	-1.98	-1.98	30.33
ILE	CG1	244	-2.14	-40.57	28.08	:	ILE	CD1	244	-1.32	-1.32	27.55
ILE	C	244	-4.58	-40.84	30.91	:	ILE	O	244	-5.32	-5.32	30.80
GLU	N	245	-4.45	-41.43	32.09	:	GLU	CA	245	-5.05	-5.05	33.27
GLU	CB	245	-6.16	-41.71	33.72	:	GLU	CG	245	-5.74	-5.74	33.88
GLU	CD	245	-6.95	-44.08	34.13	:	GLU	OE1	245	-6.88	-6.88	34.98
GLU	OE2	245	-7.98	-43.78	33.45	:	GLU	C	245	-3.96	-3.96	34.31
GLU	O	245	-3.11	-41.63	34.40	:	MET	N	246	-3.86	-3.86	35.02
MET	CA	246	-2.83	-39.38	35.98	:	MET	CB	246	-1.90	-1.90	35.55
MET	CG	246	-0.94	-38.81	34.55	:	MET	SD	246	-0.39	-0.39	33.59
MET	CE	246	0.79	-36.91	34.78	:	MET	C	246	-3.49	-3.49	37.20
MET	O	246	-4.41	-38.01	36.96	:	GLU	N	247	-3.19	-3.19	38.46
GLU	CA	247	-3.96	-38.40	39.44	:	GLU	CB	247	-4.65	-4.65	40.32
GLU	CG	247	-4.18	-40.09	41.64	:	GLU	CD	247	-2.68	-2.68	41.69

FIG. 1·17.

GLU	OE1	247	-2.11	-40.54	42.82	:	GLU	OE2	247	-2.13	-2.13	40.57
GLU	C	247	-2.96	-37.51	40.08	:	GLU	O	247	-1.77	-1.77	39.82
GLU	N	248	-3.51	-36.50	40.72	:	GLU	CA	248	-2.82	-2.82	41.20
GLU	CB	248	-3.65	-34.79	42.35	:	GLU	CG	248	-3.07	-3.07	43.28
GLU	CD	248	-4.14	-32.94	44.08	:	GLU	OE1	248	-5.20	-5.20	44.51
GLU	OE2	248	-3.88	-31.72	44.27	:	GLU	C	248	-1.35	-1.35	41.57
GLU	O	248	-0.97	-36.26	42.30	:	GLY	N	249	-0.42	-0.42	41.09
GLY	CA	249	0.96	-34.71	41.50	:	GLY	C	249	1.77	1.77	40.56
GLY	O	249	2.96	-35.28	40.42	:	ALA	N	250	1.24	1.24	39.88
ALA	CA	250	2.03	-37.48	39.00	:	ALA	CB	250	1.18	1.18	38.34
ALA	C	250	2.71	-36.73	37.89	:	ALA	O	250	2.20	2.20	37.49
LEU	N	251	3.81	-37.20	37.35	:	LEU	CA	251	4.54	4.54	36.34
LEU	CB	251	5.85	-36.07	36.91	:	LEU	CG	251	6.99	6.99	36.05
LEU	CD1	251	6.59	-34.20	35.53	:	LEU	CD2	251	8.27	8.27	36.84
LEU	C	251	4.74	-37.53	35.25	:	LEU	O	251	5.11	5.11	35.57
PHE	N	252	4.47	-37.25	33.99	:	PHE	CA	252	4.76	4.76	32.91
PHE	CB	252	3.79	-37.91	31.78	:	PHE	CG	252	3.68	3.68	30.67
PHE	CD1	252	4.70	-39.84	30.39	:	PHE	CD2	252	2.50	2.50	29.97
PHE	CE1	252	4.55	-40.79	29.40	:	PHE	CE2	252	2.38	2.38	28.98
PHE	CZ	252	3.40	-40.84	28.68	:	PHE	C	252	6.14	6.14	32.60
PHE	O	252	6.27	-36.50	32.10	:	VAL	N	253	7.19	7.19	32.89
VAL	CA	253	8.57	-37.94	32.78	:	VAL	CB	253	9.53	9.53	33.26
VAL	CG1	253	9.21	-39.42	34.70	:	VAL	CG2	253	9.42	9.42	32.40
VAL	C	253	8.95	-37.45	31.39	:	VAL	O	253	8.31	8.31	30.43
PRO	N	254	9.93	-36.54	31.20	:	PRO	CD	254	10.71	10.71	32.26
PRO	CA	254	10.42	-36.11	29.89	:	PRO	CB	254	11.78	11.78	30.26
PRO	CG	254	11.57	-34.89	31.58	:	PRO	C	254	10.45	10.45	28.83
PRO	O	254	11.05	-38.25	29.06	:	HIS	N	255	9.80	9.80	27.69
HIS	CA	255	9.87	-38.26	26.73	:	HIS	CB	255	8.84	8.84	27.08
HIS	CG	255	7.43	-38.77	27.09	:	HIS	CD2	255	6.45	6.45	26.17
HIS	ND1	255	6.93	-38.04	28.04	:	HIS	CE1	255	5.69	5.69	27.74
HIS	NE2	255	5.40	-38.35	26.62	:	HIS	C	255	9.56	9.56	25.37
HIS	O	255	9.27	-36.52	25.28	:	TYR	N	256	9.55	9.55	24.32
TYR	CA	256	9.08	-38.01	23.04	:	TYR	CB	256	10.21	10.21	22.34
TYR	CG	256	11.40	-38.11	21.88	:	TYR	CD1	256	11.27	11.27	20.88
TYR	CE1	256	12.33	-39.72	20.42	:	TYR	CD2	256	12.61	12.61	22.44
TYR	CE2	256	13.68	-38.57	21.99	:	TYR	CZ	256	13.52	13.52	20.99
TYR	OH	256	14.56	-40.24	20.59	:	TYR	C	256	8.58	8.58	22.21
TYR	O	256	8.97	-40.27	22.55	:	TYR	N	257	7.79	7.79	21.15
TYR	CA	257	7.34	-40.12	20.32	:	TYR	CB	257	5.86	5.86	19.99
TYR	CG	257	4.86	-40.41	21.02	:	TYR	CD1	257	3.71	3.71	20.65
TYR	CE1	257	2.86	-41.66	21.60	:	TYR	CD2	257	5.14	5.14	22.36
TYR	CE2	257	4.32	-40.86	23.32	:	TYR	CZ	257	3.20	3.20	22.93
TYR	OH	257	2.53	-42.22	23.92	:	TYR	C	257	8.23	8.23	19.09
TYR	O	257	8.48	-38.75	18.80	:	SER	N	258	8.86	8.86	18.38
SER	CA	258	9.60	-40.42	17.19	:	SER	CB	258	10.56	10.56	16.90
SER	OG	258	9.98	-42.77	16.94	:	SER	C	258	8.61	8.61	16.09
SER	O	258	7.73	-41.10	16.16	:	LYS	N	259	8.51	8.51	15.05
LYS	CA	259	7.40	-39.58	14.06	:	LYS	CB	259	7.72	7.72	13.01
LYS	CG	259	8.02	-42.13	13.44	:	LYS	CD	259	7.88	7.88	12.29
LYS	CE	259	6.51	-43.06	11.68	:	LYS	NZ	259	5.57	5.57	12.77
LYS	C	259	6.00	-39.89	14.53	:	LYS	O	259	5.56	5.56	14.37
ALA	N	260	5.27	-39.02	15.20	:	ALA	CA	260	3.86	3.86	15.59
ALA	CB	260	3.68	-40.36	16.65	:	ALA	C	260	3.42	3.42	16.21
ALA	O	260	3.93	-37.52	17.24	:	ILE	N	261	2.55	2.55	15.53
ILE	CA	261	2.17	-35.88	16.01	:	ILE	CB	261	1.81	1.81	14.80
ILE	CG2	261	1.32	-33.71	15.25	:	ILE	CG1	261	2.99	2.99	13.92
ILE	CD1	261	2.54	-34.49	12.57	:	ILE	C	261	1.00	1.00	16.92
ILE	O	261	0.04	-36.72	16.40	:	VAL	N	262	1.05	1.05	18.22

FIG. 1·18.

VAL	CA	262	-0.01	-36.27	19.14	:	VAL	CB	262	0.64	0.64	20.39
VAL	CG1	262	-0.32	-36.96	21.50	:	VAL	CG2	262	1.28	1.28	20.07
VAL	C	262	-0.80	-35.03	19.38	:	VAL	O	262	-0.20	-0.20	19.65
ILE	N	263	-2.10	-35.06	19.21	:	ILE	CA	263	-2.99	-2.99	19.50
ILE	CB	263	-4.14	-33.89	18.46	:	ILE	CG2	263	-5.06	-5.06	18.81
ILE	CG1	263	-3.62	-33.72	17.05	:	ILE	CD1	263	-4.65	-4.65	15.97
ILE	C	263	-3.52	-34.41	20.86	:	ILE	O	263	-4.12	-4.12	20.88
LEU	N	264	-3.26	-33.74	22.00	:	LEU	CA	264	-3.71	-3.71	23.32
LEU	CB	264	-2.75	-33.85	24.43	:	LEU	CG	264	-1.82	-1.82	25.11
LEU	CD1	264	-1.72	-34.21	26.49	:	LEU	CD2	264	-2.30	-2.30	25.23
LEU	C	264	-4.87	-33.28	23.67	:	LEU	O	264	-4.68	-4.68	23.58
VAL	N	265	-6.02	-33.78	24.07	:	VAL	CA	265	-7.12	-7.12	24.48
VAL	CB	265	-8.35	-33.09	23.50	:	VAL	CG1	265	-8.33	-8.33	22.79
VAL	CG2	265	-9.66	-32.99	24.23	:	VAL	C	265	-7.40	-7.40	25.90
VAL	O	265	-7.44	-34.57	26.21	:	VAL	N	266	-7.52	-7.52	26.81
VAL	CA	266	-7.68	-32.81	28.19	:	VAL	CB	266	-6.89	-6.89	29.18
VAL	CG1	266	-6.24	-30.77	28.44	:	VAL	CG2	266	-7.75	-7.75	30.22
VAL	C	266	-9.18	-32.85	28.40	:	VAL	O	266	-9.93	-9.93	27.81
ASN	N	267	-9.63	-33.82	29.17	:	ASN	CA	267	-11.03	-11.03	29.32
ASN	CB	267	-11.28	-35.55	29.20	:	ASN	CG	267	-11.24	-11.24	27.78
ASN	OD1	267	-11.63	-35.27	26.90	:	ASN	ND2	267	-10.83	-10.83	27.45
ASN	C	267	-11.79	-33.61	30.54	:	ASN	O	267	-12.95	-12.95	30.37
GLU	N	268	-11.17	-33.91	31.69	:	GLU	CA	268	-11.61	-11.61	33.09
GLU	CB	268	-12.21	-35.12	33.67	:	GLU	CG	268	-12.50	-12.50	35.19
GLU	CD	268	-11.48	-36.55	36.05	:	GLU	OE1	268	-10.45	-10.45	36.58
GLU	OE2	268	-11.73	-37.79	36.22	:	GLU	C	268	-10.24	-10.24	33.68
GLU	O	268	-9.30	-34.20	33.40	:	GLY	N	269	-10.03	-10.03	34.31
GLY	CA	269	-8.82	-32.06	35.10	:	GLY	C	269	-7.95	-7.95	34.72
GLY	O	269	-8.19	-30.31	33.69	:	GLU	N	270	-6.95	-6.95	35.51
GLU	CA	270	-5.97	-29.54	35.18	:	GLU	CB	270	-5.85	-5.85	36.21
GLU	CG	270	-6.99	-27.51	36.38	:	GLU	CD	270	-8.27	-8.27	36.78
GLU	OE1	270	-8.33	-28.86	37.85	:	GLU	OE2	270	-9.21	-9.21	35.97
GLU	C	270	-4.56	-30.12	35.05	:	GLU	O	270	-4.22	-4.22	35.74
ALA	N	271	-3.61	-29.65	34.25	:	ALA	CA	271	-2.29	-2.29	34.19
ALA	CB	271	-2.18	-31.38	33.19	:	ALA	C	271	-1.33	-1.33	33.72
ALA	O	271	-1.76	-28.26	33.11	:	HIS	N	272	-0.03	-0.03	33.90
HIS	CA	272	0.89	-28.27	33.49	:	HIS	CB	272	1.63	1.63	34.72
HIS	CG	272	2.91	-27.25	34.41	:	HIS	CD2	272	3.11	3.11	34.59
HIS	ND1	272	4.00	-27.75	33.88	:	HIS	CE1	272	4.84	4.84	33.72
HIS	NE2	272	4.29	-25.68	34.16	:	HIS	C	272	1.72	1.72	32.44
HIS	O	272	2.20	-30.06	32.76	:	VAL	N	273	2.03	2.03	31.24
VAL	CA	273	2.79	-29.24	30.27	:	VAL	CB	273	1.88	1.88	29.05
VAL	CG1	273	1.40	-28.30	28.43	:	VAL	CG2	273	2.64	2.64	28.01
VAL	C	273	4.01	-28.44	29.88	:	VAL	O	273	3.99	3.99	30.12
GLU	N	274	5.13	-29.03	29.46	:	GLU	CA	274	6.27	6.27	29.00
GLU	CB	274	7.44	-28.24	29.97	:	GLU	CG	274	7.10	7.10	31.43
GLU	CD	274	8.08	-27.57	32.31	:	GLU	OE1	274	7.64	7.64	33.08
GLU	OE2	274	9.30	-27.79	32.23	:	GLU	C	274	6.77	6.77	27.79
GLU	O	274	7.00	-30.21	27.91	:	LEU	N	275	6.91	6.91	26.63
LEU	CA	275	7.31	-28.97	25.36	:	LEU	CB	275	6.29	6.29	24.33
LEU	CG	275	5.93	-29.14	23.02	:	LEU	CD1	275	6.27	6.27	21.89
LEU	CD2	275	6.65	-30.43	22.88	:	LEU	C	275	8.66	8.66	25.11
LEU	O	275	8.77	-27.19	25.43	:	VAL	N	276	9.70	9.70	24.59
VAL	CA	276	10.96	-28.38	24.29	:	VAL	CB	276	12.15	12.15	24.89
VAL	CG1	276	13.50	-28.55	24.44	:	VAL	CG2	276	12.07	12.07	26.39
VAL	C	276	11.13	-28.34	22.80	:	VAL	O	276	11.17	11.17	22.09
GLY	N	277	11.26	-27.16	22.28	:	GLY	CA	277	11.22	11.22	20.83
GLY	C	277	12.42	-26.27	20.32	:	GLY	O	277	13.19	13.19	21.14
PRO	N	278	12.68	-26.17	19.03	:	PRO	CD	278	11.91	11.91	18.00

FIG. 1·19.

PRO	CA	278	13.80	-25.39	18.52	:	PRO	CB	278	14.14	14.14	17.23
PRO	CG	278	12.73	-26.38	16.77	:	PRO	C	278	13.26	13.26	18.44
PRO	O	278	12.09	-23.75	18.13	:	LYS	N	279	14.11	14.11	18.72
LYS	CA	279	13.66	-21.64	18.99	:	LYS	CB	279	14.85	14.85	19.60
LYS	CG	279	14.66	-19.49	19.77	:	LYS	CD	279	16.02	16.02	19.78
LYS	CE	279	16.41	-18.44	21.24	:	LYS	NZ	279	17.10	17.10	21.89
LYS	C	279	13.20	-21.04	17.69	:	LYS	O	279	13.98	13.98	16.75
GLY	N	280	11.90	-20.86	17.59	:	GLY	CA	280	11.24	11.24	16.37
GLY	C	280	11.56	-21.30	15.08	:	GLY	O	280	10.83	10.83	14.18
ASN	N	281	12.45	-22.36	14.82	:	ASN	CA	281	12.77	12.77	13.45
ASN	CB	281	12.81	-21.85	12.40	:	ASN	CG	281	14.20	14.20	12.42
ASN	OD1	281	14.83	-21.15	11.34	:	ASN	ND2	281	14.72	14.72	13.59
ASN	C	281	14.12	-23.72	13.19	:	ASN	O	281	15.01	15.01	14.01
LYS	N	282	14.30	-24.10	11.91	:	LYS	CA	282	15.44	15.44	11.26
LYS	CB	282	15.23	-25.00	9.67	:	LYS	CG	282	16.16	16.16	8.76
LYS	CD	282	17.00	-24.72	8.02	:	LYS	CE	282	18.57	18.57	8.21
LYS	NZ	282	19.33	-23.53	7.97	:	LYS	C	282	16.70	16.70	11.48
LYS	O	282	16.64	-22.86	11.65	:	GLU	N	283	17.86	17.86	11.42
GLU	CA	283	19.14	-24.13	11.85	:	GLU	CB	283	19.57	19.57	11.17
GLU	CG	283	21.12	-22.73	10.94	:	GLU	CD	283	22.08	22.08	11.97
GLU	OE1	283	22.70	-20.97	11.49	:	GLU	OE2	283	22.25	22.25	13.19
GLU	C	283	18.86	-23.83	13.33	:	GLU	O	283	17.81	17.81	13.82
THR	N	284	19.65	-23.13	14.13	:	THR	CA	284	19.43	19.43	15.55
THR	CB	284	18.09	-22.43	15.86	:	THR	OG1	284	18.62	18.62	16.54
THR	CG2	284	16.99	-23.14	16.65	:	THR	C	284	19.47	19.47	16.10
THR	O	284	18.84	-25.55	15.77	:	LEU	N	285	20.51	20.51	16.90
LEU	CA	285	20.65	-25.71	17.81	:	LEU	CB	285	22.14	22.14	17.86
LEU	CG	285	22.68	-27.39	17.30	:	LEU	CD1	285	22.18	22.18	15.97
LEU	CD2	285	24.13	-27.12	17.10	:	LEU	C	285	20.13	20.13	19.10
LEU	O	285	20.42	-25.57	20.19	:	GLU	N	286	19.44	19.44	19.07
GLU	CA	286	18.88	-23.32	20.26	:	GLU	CB	286	18.70	18.70	20.15
GLU	CG	286	19.99	-21.12	20.00	:	GLU	CD	286	19.72	19.72	20.39
GLU	OE1	286	19.72	-19.45	21.61	:	GLU	OE2	286	19.34	19.34	19.54
GLU	C	286	17.49	-23.85	20.58	:	GLU	O	286	16.60	16.60	19.79
TYR	N	287	17.27	-24.58	21.68	:	TYR	CA	287	15.94	15.94	22.10
TYR	CB	287	16.08	-26.36	22.91	:	TYR	CG	287	16.93	16.93	22.16
TYR	CD1	287	18.18	-27.70	22.64	:	TYR	CE1	287	19.06	19.06	21.90
TYR	CD2	287	16.51	-27.79	20.94	:	TYR	CE2	287	17.36	17.36	20.18
TYR	CZ	287	18.64	-28.84	20.64	:	TYR	OH	287	19.55	19.55	19.74
TYR	C	287	15.31	-23.94	22.94	:	TYR	O	287	15.99	15.99	23.19
GLU	N	288	14.03	-23.98	23.26	:	GLU	CA	288	13.35	13.35	23.99
GLU	CB	288	13.12	-21.89	22.99	:	GLU	CG	288	12.36	12.36	23.42
GLU	CD	288	11.21	-20.47	22.42	:	GLU	OE1	288	10.21	10.21	22.64
GLU	OE2	288	11.35	-19.69	21.43	:	GLU	C	288	12.09	12.09	24.50
GLU	O	288	11.59	-24.35	23.70	:	SER	N	289	11.54	11.54	25.70
SER	CA	289	10.34	-24.20	25.99	:	SER	CB	289	10.39	10.39	27.30
SER	OG	289	10.80	-24.25	28.45	:	SER	C	289	9.05	9.05	26.02
SER	O	289	8.98	-22.35	26.51	:	TYR	N	290	8.02	8.02	25.56
TYR	CA	290	6.65	-23.72	25.39	:	TYR	CB	290	6.13	6.13	24.04
TYR	CG	290	7.03	-23.76	22.91	:	TYR	CD1	290	6.71	6.71	22.20
TYR	CE1	290	7.52	-22.22	21.17	:	TYR	CD2	290	8.15	8.15	22.57
TYR	CE2	290	8.96	-24.07	21.55	:	TYR	CZ	290	8.64	8.64	20.87
TYR	OH	290	9.50	-22.46	19.92	:	TYR	C	290	5.91	5.91	26.55
TYR	O	290	5.68	-25.60	26.56	:	ARG	N	291	5.68	5.68	27.65
ARG	CA	291	5.03	-24.32	28.76	:	ARG	CB	291	5.68	5.68	30.03
ARG	CG	291	7.20	-23.95	30.12	:	ARG	CD	291	7.60	7.60	31.54
ARG	NE	291	9.03	-23.39	31.87	:	ARG	CZ	291	10.04	10.04	31.53
ARG	NH1	291	11.30	-23.90	31.88	:	ARG	NH2	291	9.85	9.85	30.84
ARG	C	291	3.60	-23.85	28.61	:	ARG	O	291	3.39	3.39	27.95

FIG. 1.20.

ALA	N	292	2.59	-24.46	29.19	:	ALA	CA	292	1.24	1.24	29.05
ALA	CB	292	0.67	-24.41	27.71	:	ALA	C	292	0.47	0.47	30.16
ALA	O	292	0.88	-25.75	30.61	:	GLU	N	293	-0.68	-0.68	30.56
GLU	CA	293	-1.37	-24.66	31.72	:	GLU	CB	293	-1.55	-1.55	32.63
GLU	CG	293	-1.15	-23.76	34.03	:	GLU	CD	293	0.33	0.33	34.25
GLU	OE1	293	1.24	-23.67	33.53	:	GLU	OE2	293	0.58	0.58	35.22
GLU	C	293	-2.69	-25.20	31.25	:	GLU	O	293	-3.59	-3.59	31.06
LEU	N	294	-2.84	-26.51	31.07	:	LEU	CA	294	-4.00	-4.00	30.43
LEU	CB	294	-3.60	-28.50	29.90	:	LEU	CG	294	-2.38	-2.38	29.09
LEU	CD1	294	-2.27	-29.95	28.48	:	LEU	CD2	294	-2.48	-2.48	27.98
LEU	C	294	-5.21	-27.35	31.32	:	LEU	O	294	-5.01	-5.01	32.50
SER	N	295	-6.45	-27.24	30.87	:	SER	CA	295	-7.63	-7.63	31.67
SER	CB	295	-7.96	-26.24	32.42	:	SER	OG	295	-7.99	-7.99	31.58
SER	C	295	-8.81	-27.99	30.83	:	SER	O	295	-8.76	-8.76	29.61
LYS	N	296	-9.95	-28.41	31.35	:	LYS	CA	296	-11.03	-11.03	30.63
LYS	CB	296	-12.41	-28.73	31.14	:	LYS	CG	296	-13.22	-13.22	31.39
LYS	CD	296	-14.71	-29.79	31.59	:	LYS	CE	296	-15.43	-15.43	30.32
LYS	NZ	296	-14.55	-29.69	29.16	:	LYS	C	296	-11.26	-11.26	29.17
LYS	O	296	-11.99	-29.98	28.86	:	ASP	N	297	-10.97	-10.97	28.22
ASP	CA	297	-11.14	-28.58	26.81	:	ASP	CB	297	-12.38	-12.38	26.27
ASP	CG	297	-13.48	-29.07	26.25	:	ASP	OD1	297	-14.59	-14.59	26.57
ASP	OD2	297	-13.29	-30.26	25.97	:	ASP	C	297	-10.03	-10.03	25.95
ASP	O	297	-10.20	-27.58	24.81	:	ASP	N	298	-8.87	-8.87	26.55
ASP	CA	298	-7.72	-27.36	25.91	:	ASP	CB	298	-6.72	-6.72	26.93
ASP	CG	298	-6.97	-25.69	27.70	:	ASP	OD1	298	-6.35	-6.35	28.71
ASP	OD2	298	-7.78	-24.88	27.33	:	ASP	C	298	-7.11	-7.11	25.05
ASP	O	298	-7.13	-29.58	25.43	:	VAL	N	299	-6.50	-6.50	23.93
VAL	CA	299	-5.80	-29.17	23.26	:	VAL	CB	299	-6.45	-6.45	21.85
VAL	CG1	299	-7.82	-29.01	21.71	:	VAL	CG2	299	-5.55	-5.55	20.72
VAL	C	299	-4.41	-28.63	23.13	:	VAL	O	299	-4.21	-4.21	22.92
PHE	N	300	-3.41	-29.44	23.33	:	PHE	CA	300	-2.03	-2.03	23.18
PHE	CB	300	-1.28	-29.24	24.50	:	PHE	CG	300	0.12	0.12	24.53
PHE	CD1	300	0.35	-27.31	24.88	:	PHE	CD2	300	1.21	1.21	24.23
PHE	CE1	300	1.62	-26.80	24.93	:	PHE	CE2	300	2.47	2.47	24.28
PHE	CZ	300	2.69	-27.57	24.63	:	PHE	C	300	-1.52	-1.52	22.12
PHE	O	300	-1.88	-31.17	22.32	:	VAL	N	301	-0.80	-0.80	21.03
VAL	CA	301	-0.27	-30.61	20.06	:	VAL	CB	301	-0.58	-0.58	18.58
VAL	CG1	301	-0.81	-28.75	18.48	:	VAL	CG2	301	0.56	0.56	17.63
VAL	C	301	1.22	-30.66	20.34	:	VAL	O	301	1.86	1.86	20.56
ILE	N	302	1.78	-31.85	20.41	:	ILE	CA	302	3.16	3.16	20.76
ILE	CB	302	3.16	-33.28	21.83	:	ILE	CG2	302	4.57	4.57	22.25
ILE	CG1	302	2.38	-32.90	23.07	:	ILE	CD1	302	1.85	1.85	23.87
ILE	C	302	3.72	-32.58	19.41	:	ILE	O	302	3.25	3.25	18.95
PRO	N	303	4.58	-31.85	18.68	:	PRO	CD	303	5.09	5.09	19.04
PRO	CA	303	5.10	-32.20	17.36	:	PRO	CB	303	5.91	5.91	16.97
PRO	CG	303	5.32	-29.90	17.71	:	PRO	C	303	5.88	5.88	17.37
PRO	O	303	5.68	-34.23	18.33	:	ALA	N	304	6.81	6.81	16.46
ALA	CA	304	7.25	-35.21	16.55	:	ALA	CB	304	6.95	6.95	15.21
ALA	C	304	8.60	-35.63	17.01	:	ALA	O	304	8.85	8.85	16.82
ALA	N	305	9.64	-34.97	17.44	:	ALA	CA	305	10.64	10.64	18.28
ALA	CB	305	12.02	-35.52	17.84	:	ALA	C	305	10.35	10.35	19.42
ALA	O	305	9.23	-34.88	19.91	:	TYR	N	306	11.08	11.08	19.97
TYR	CA	306	10.44	-32.79	20.87	:	TYR	CB	306	9.17	9.17	20.31
TYR	CG	306	9.27	-31.02	19.19	:	TYR	CD1	306	9.69	9.69	17.93
TYR	CE1	306	9.72	-30.55	16.86	:	TYR	CD2	306	8.86	8.86	19.41
TYR	CE2	306	8.89	-28.88	18.34	:	TYR	CZ	306	9.31	9.31	17.09
TYR	OH	306	9.30	-28.45	15.98	:	TYR	C	306	9.97	9.97	22.20
TYR	O	306	8.89	-33.85	22.35	:	PRO	N	307	10.80	10.80	23.19
PRO	CD	307	12.15	-32.69	23.06	:	PRO	CA	307	10.54	10.54	24.52

FIG. 1.21.

						:						
PRO	CB	307	11.80	-33.33	25.21	:	PRO	CG	307	12.77	12.77	24.08
PRO	C	307	9.32	-33.05	25.17	:	PRO	O	307	9.21	9.21	25.13
VAL	N	308	8.39	-33.77	25.75	:	VAL	CA	308	7.27	7.27	26.42
VAL	CB	308	6.01	-33.42	25.57	:	VAL	CG1	308	5.74	5.74	25.61
VAL	CG2	308	4.79	-32.68	26.06	:	VAL	C	308	7.25	7.25	27.82
VAL	O	308	7.74	-34.81	28.01	:	ALA	N	309	6.75	6.75	28.87
ALA	CA	309	6.69	-33.65	30.23	:	ALA	CB	309	7.77	7.77	31.14
ALA	C	309	5.39	-33.11	30.74	:	ALA	O	309	5.20	5.20	30.59
ILE	N	310	4.46	-33.89	31.25	:	ILE	CA	310	3.13	3.13	31.58
ILE	CB	310	2.07	-34.28	30.92	:	ILE	CG2	310	0.69	0.69	31.29
ILE	CG1	310	2.15	-34.13	29.44	:	ILE	CD1	310	1.19	1.19	28.63
ILE	C	310	3.03	-33.51	33.08	:	ILE	O	310	3.40	3.40	33.58
LYS	N	311	2.66	-32.55	33.90	:	LYS	CA	311	2.46	2.46	35.32
LYS	CB	311	3.29	-31.81	36.09	:	LYS	CG	311	2.97	2.97	37.54
LYS	CD	311	4.15	-31.35	38.33	:	LYS	CE	311	3.63	3.63	39.75
LYS	NZ	311	2.99	-32.32	40.26	:	LYS	C	311	1.00	1.00	35.69
LYS	O	311	0.39	-31.60	35.38	:	ALA	N	312	0.38	0.38	36.35
ALA	CA	312	-1.00	-33.42	36.74	:	ALA	CB	312	-1.58	-1.58	37.09
ALA	C	312	-1.10	-32.53	37.95	:	ALA	O	312	-0.30	-0.30	38.88
THR	N	313	-2.06	-31.65	37.94	:	THR	CA	313	-2.25	-2.25	38.93
THR	CB	313	-2.45	-29.36	38.12	:	THR	OG1	313	-1.14	-1.14	38.02
THR	CG2	313	-3.30	-28.26	38.69	:	THR	C	313	-3.43	-3.43	39.79
THR	O	313	-3.54	-30.58	40.93	:	SER	N	314	-4.38	-4.38	39.17
SER	CA	314	-5.50	-32.33	39.78	:	SER	CB	314	-6.65	-6.65	39.50
SER	OG	314	-6.57	-30.97	38.19	:	SER	C	314	-5.57	-5.57	39.08
SER	O	314	-4.72	-33.96	38.25	:	ASN	N	315	-6.49	-6.49	39.33
ASN	CA	315	-6.57	-35.81	38.58	:	ASN	CB	315	-7.58	-7.58	39.17
ASN	CG	315	-7.24	-37.18	40.58	:	ASN	OD1	315	-6.32	-6.32	41.20
ASN	ND2	315	-7.91	-38.13	41.20	:	ASN	C	315	-7.07	-7.07	37.24
ASN	O	315	-7.97	-34.52	37.22	:	VAL	N	316	-6.47	-6.47	36.18
VAL	CA	316	-6.80	-35.46	34.86	:	VAL	CB	316	-5.62	-5.62	34.63
VAL	CG1	316	-4.31	-35.18	34.63	:	VAL	CG2	316	-5.89	-5.89	33.38
VAL	C	316	-7.01	-36.58	33.85	:	VAL	O	316	-6.33	-6.33	33.93
ASN	N	317	-7.91	-36.52	32.89	:	ASN	CA	317	-8.00	-8.00	31.92
ASN	CB	317	-9.37	-38.10	31.75	:	ASN	CG	317	-9.95	-9.95	33.07
ASN	OD1	317	-9.26	-39.33	33.77	:	ASN	ND2	317	-11.21	-11.21	33.48
ASN	C	317	-7.64	-37.02	30.59	:	ASN	O	317	-8.31	-8.31	30.27
PHE	N	318	-6.70	-37.49	29.78	:	PHE	CA	318	-6.47	-6.47	28.48
PHE	CB	318	-4.98	-36.68	28.31	:	PHE	CG	318	-4.26	-4.26	29.28
PHE	CD1	318	-3.62	-36.26	30.38	:	PHE	CD2	318	-4.21	-4.21	29.06
PHE	CE1	318	-2.92	-35.45	31.24	:	PHE	CE2	318	-3.51	-3.51	29.92
PHE	CZ	318	-2.86	-34.11	31.02	:	PHE	C	318	-6.99	-6.99	27.42
PHE	O	318	-7.07	-39.09	27.75	:	THR	N	319	-7.43	-7.43	26.20
THR	CA	319	-7.67	-38.51	25.11	:	THR	CB	319	-9.01	-9.01	24.39
THR	OG1	319	-10.05	-38.69	25.25	:	THR	CG2	319	-9.11	-9.11	23.17
THR	C	319	-6.57	-38.07	24.14	:	THR	O	319	-6.54	-6.54	23.90
GLY	N	320	-5.65	-38.85	23.60	:	GLY	CA	320	-4.68	-4.68	22.68
GLY	C	320	-4.95	-38.90	21.33	:	GLY	O	320	-5.44	-5.44	21.33
PHE	N	321	-4.78	-38.28	20.16	:	PHE	CA	321	-4.89	-4.89	18.89
PHE	CB	321	-5.82	-38.32	17.89	:	PHE	CG	321	-7.25	-7.25	18.34
PHE	CD1	321	-7.95	-39.55	18.24	:	PHE	CD2	321	-7.86	-7.86	18.90
PHE	CE1	321	-9.23	-39.65	18.68	:	PHE	CE2	321	-9.14	-9.14	19.35
PHE	CZ	321	-9.82	-38.56	19.25	:	PHE	C	321	-3.49	-3.49	18.34
PHE	O	321	-2.99	-37.74	18.37	:	GLY	N	322	-2.73	-2.73	17.90
GLY	CA	322	-1.38	-39.59	17.41	:	GLY	C	322	-1.47	-1.47	15.93
GLY	O	322	-1.76	-40.92	15.49	:	ILE	N	323	-1.34	-1.34	15.10
ILE	CA	323	-1.45	-38.99	13.66	:	ILE	CB	323	-1.89	-1.89	12.89
ILE	CG2	323	-3.00	-36.95	13.62	:	ILE	CG1	323	-0.74	-0.74	12.73
ILE	CD1	323	-0.26	-36.78	11.28	:	ILE	C	323	-0.06	-0.06	13.27

FIG. 1.22

ILE	O	323	0.91	-39.08	13.95	:	ASN	N	324	0.08	0.08	12.18
ASN	CA	324	1.36	-40.63	11.66	:	ASN	CB	324	2.32	2.32	11.49
ASN	CG	324	3.61	-39.91	10.86	:	ASN	OD1	324	4.72	4.72	11.41
ASN	ND2	324	3.45	-40.56	9.72	:	ASN	C	324	1.97	1.97	12.57
ASN	O	324	3.16	-41.93	12.70	:	ALA	N	325	1.19	1.19	13.06
ALA	CA	325	1.65	-43.50	14.07	:	ALA	CB	325	0.47	0.47	14.92
ALA	C	325	2.38	-44.76	13.70	:	ALA	O	325	2.94	2.94	14.62
ASN	N	326	2.55	-45.29	12.47	:	ASN	CA	326	3.12	3.12	12.32
ASN	CB	326	2.82	-47.23	10.93	:	ASN	CG	326	1.29	1.29	10.67
ASN	OD1	326	0.87	-47.01	9.56	:	ASN	ND2	326	0.34	0.34	11.60
ASN	C	326	4.61	-46.70	12.58	:	ASN	O	326	5.38	5.38	12.23
ASN	N	327	4.98	-47.71	13.34	:	ASN	CA	327	6.33	6.33	13.83
ASN	CB	327	7.35	-47.99	12.71	:	ASN	CG	327	6.95	6.95	11.65
ASN	OD1	327	6.82	-50.20	11.92	:	ASN	ND2	327	6.69	6.69	10.43
ASN	C	327	6.72	-46.68	14.64	:	ASN	O	327	7.84	7.84	14.55
ASN	N	328	5.77	-46.08	15.35	:	ASN	CA	328	6.10	6.10	16.19
ASN	CB	328	4.82	-44.35	16.70	:	ASN	CG	328	5.09	5.09	17.74
ASN	OD1	328	5.90	-42.44	17.53	:	ASN	ND2	328	4.55	4.55	18.93
ASN	C	328	6.97	-45.47	17.33	:	ASN	O	328	6.94	6.94	17.50
ASN	N	329	7.67	-44.78	18.22	:	ASN	CA	329	8.52	8.52	19.22
ASN	CB	329	9.89	-45.51	18.73	:	ASN	CG	329	10.32	10.32	18.55
ASN	OD1	329	9.58	-47.73	18.07	:	ASN	ND2	329	11.54	11.54	18.93
ASN	C	329	8.55	-44.47	20.37	:	ASN	O	329	9.04	9.04	20.21
ARG	N	330	8.14	-44.86	21.55	:	ARG	CA	330	7.98	7.98	22.62
ARG	CB	330	6.89	-44.41	23.51	:	ARG	CG	330	6.19	6.19	24.26
ARG	CD	330	5.11	-43.97	25.14	:	ARG	NE	330	4.07	4.07	24.44
ARG	CZ	330	3.99	-46.12	24.50	:	ARG	NH1	330	2.99	2.99	23.89
ARG	NH2	330	4.91	-46.84	25.15	:	ARG	C	330	9.31	9.31	23.32
ARG	O	330	9.70	-44.80	23.86	:	ASN	N	331	10.09	10.09	23.31
ASN	CA	331	11.41	-42.77	23.94	:	ASN	CB	331	12.37	12.37	23.12
ASN	CG	331	12.74	-42.83	21.95	:	ASN	OD1	331	13.78	13.78	22.03
ASN	ND2	331	12.06	-43.07	20.83	:	ASN	C	331	11.38	11.38	25.30
ASN	O	331	11.03	-40.96	25.28	:	LEU	N	332	11.64	11.64	26.46
LEU	CA	332	11.57	-42.06	27.71	:	LEU	CB	332	10.95	10.95	28.72
LEU	CG	332	9.51	-42.60	28.75	:	LEU	CD1	332	8.74	8.74	27.67
LEU	CD2	332	9.00	-43.07	30.05	:	LEU	C	332	12.92	12.92	28.17
LEU	O	332	13.92	-42.19	27.84	:	LEU	N	333	13.02	13.02	28.84
LEU	CA	333	14.30	-39.89	29.27	:	LEU	CB	333	14.40	14.40	28.84
LEU	CG	333	14.11	-38.13	27.39	:	LEU	CD1	333	13.99	13.99	27.22
LEU	CD2	333	15.19	-38.68	26.51	:	LEU	C	333	14.51	14.51	30.78
LEU	O	333	15.45	-39.45	31.34	:	ALA	N	334	13.69	13.69	31.52
ALA	CA	334	13.88	-40.85	32.93	:	ALA	CB	334	13.17	13.17	33.65
ALA	C	334	13.23	-42.15	33.31	:	ALA	O	334	12.23	12.23	32.69
GLY	N	335	13.75	-42.88	34.28	:	GLY	CA	335	13.00	13.00	34.72
GLY	C	335	13.54	-45.31	34.12	:	GLY	O	335	14.56	14.56	33.42
LYS	N	336	12.87	-46.42	34.49	:	LYS	CA	336	13.33	13.33	34.04
LYS	CB	336	13.04	-48.81	35.07	:	LYS	CG	336	13.77	13.77	36.37
LYS	CD	336	14.36	-49.56	37.16	:	LYS	CE	336	13.32	13.32	37.51
LYS	NZ	336	12.17	-50.26	38.34	:	LYS	C	336	12.77	12.77	32.74
LYS	O	336	13.56	-48.46	31.84	:	THR	N	337	11.48	11.48	32.50
THR	CA	337	11.01	-48.80	31.20	:	THR	CB	337	9.55	9.55	31.29
THR	OG1	337	9.28	-49.63	32.49	:	THR	CG2	337	8.99	8.99	30.05
THR	C	337	11.36	-47.82	30.07	:	THR	O	337	11.31	11.31	30.29
ASP	N	338	11.73	-48.28	28.88	:	ASP	CA	338	12.03	12.03	27.76
ASP	CB	338	10.67	-47.02	27.23	:	ASP	CG	338	9.84	9.84	26.67
ASP	OD1	338	8.62	-48.00	26.63	:	ASP	OD2	338	10.42	10.42	26.30
ASP	C	338	12.94	-46.16	27.89	:	ASP	O	338	12.78	12.78	27.20
ASN	N	339	13.99	-46.17	28.68	:	ASN	CA	339	14.78	14.78	28.96
ASN	CB	339	15.41	-45.12	30.33	:	ASN	CG	339	16.10	16.10	30.71

FIG. 1·23.

ASN	OD1	339	15.74	-43.20	31.69	:	ASN	ND2	339	17.11	17.11	30.07
ASN	C	339	15.87	-44.71	27.95	:	ASN	O	339	17.00	17.00	28.27
VAL	N	340	15.79	-43.98	26.82	:	VAL	CA	340	16.89	16.89	25.85
VAL	CB	340	16.79	-42.96	24.73	:	VAL	CG1	340	16.23	16.23	23.70
VAL	CG2	340	16.07	-41.69	24.99	:	VAL	C	340	18.25	18.25	26.34
VAL	O	340	19.19	-44.21	25.82	:	ILE	N	341	18.36	18.36	27.36
ILE	CA	341	19.68	-42.41	27.83	:	ILE	CB	341	19.62	19.62	28.93
ILE	CG2	341	21.04	-40.91	29.38	:	ILE	CG1	341	19.00	19.00	28.36
ILE	CD1	341	19.09	-38.77	29.21	:	ILE	C	341	20.36	20.36	28.36
ILE	O	341	21.45	-43.92	27.87	:	SER	N	342	19.85	19.85	29.19
SER	CA	342	20.74	-45.65	29.60	:	SER	CB	342	20.18	20.18	30.79
SER	OG	342	18.89	-46.79	30.44	:	SER	C	342	20.95	20.95	28.51
SER	O	342	21.92	-47.44	28.58	:	SER	N	343	20.06	20.06	27.53
SER	CA	343	20.31	-47.63	26.38	:	SER	CB	343	19.10	19.10	25.46
SER	OG	343	19.17	-48.62	24.43	:	SER	C	343	21.53	21.53	25.63
SER	O	343	22.27	-47.90	25.03	:	ILE	N	344	21.78	21.78	25.64
ILE	CA	344	22.97	-45.26	24.98	:	ILE	CB	344	23.05	23.05	25.01
ILE	CG2	344	24.45	-43.29	24.58	:	ILE	CG1	344	22.02	22.02	24.09
ILE	CD1	344	22.18	-41.61	23.95	:	ILE	C	344	24.10	24.10	25.81
ILE	O	344	25.02	-46.47	25.25	:	GLY	N	345	24.01	24.01	27.15
GLY	CA	345	25.05	-46.27	28.05	:	GLY	C	345	24.85	24.85	28.29
GLY	O	345	24.69	-48.28	29.40	:	ARG	N	346	24.78	24.78	27.19
ARG	CA	346	24.63	-49.89	27.12	:	ARG	CB	346	23.20	23.20	27.33
ARG	CG	346	23.31	-51.42	28.30	:	ARG	CD	346	23.10	23.10	29.73
ARG	NE	346	21.76	-50.34	29.79	:	ARG	CZ	346	20.70	20.70	29.57
ARG	NH1	346	19.46	-50.59	29.43	:	ARG	NH2	346	20.88	20.88	29.57
ARG	C	346	25.03	-50.26	25.70	:	ARG	O	346	24.97	24.97	25.29
ALA	N	347	25.29	-49.27	24.85	:	ALA	CA	347	25.91	25.91	23.60
ALA	CB	347	25.83	-48.29	22.79	:	ALA	C	347	27.35	27.35	23.85
ALA	O	347	27.92	-49.86	24.93	:	LEU	N	348	27.98	27.98	22.82
LEU	CA	348	29.23	-51.23	22.93	:	LEU	CB	348	29.42	29.42	21.68
LEU	CG	348	30.55	-53.03	21.63	:	LEU	CD1	348	29.84	29.84	20.99
LEU	CD2	348	31.83	-52.63	20.87	:	LEU	C	348	30.24	30.24	23.02
LEU	O	348	31.01	-50.06	22.08	:	ASP	N	349	30.32	30.32	24.09
ASP	CA	349	31.11	-48.12	24.11	:	ASP	CB	349	31.23	31.23	22.75
ASP	CG	349	30.00	-47.24	21.79	:	ASP	OD1	349	28.86	28.86	22.25
ASP	OD2	349	30.17	-47.02	20.58	:	ASP	C	349	30.37	30.37	25.02
ASP	O	349	30.97	-46.23	25.60	:	GLY	N	350	29.05	29.05	25.01
GLY	CA	350	28.09	-46.70	25.85	:	GLY	C	350	28.69	28.69	26.78
GLY	O	350	28.77	-44.47	26.45	:	LYS	N	351	29.32	29.32	27.84
LYS	CA	351	29.71	-45.17	28.84	:	LYS	CB	351	30.32	30.32	30.02
LYS	CG	351	29.30	-46.71	30.78	:	LYS	CD	351	29.72	29.72	32.26
LYS	CE	351	29.38	-48.10	32.84	:	LYS	NZ	351	29.86	29.86	34.19
LYS	C	351	30.65	-44.11	28.38	:	LYS	O	351	30.50	30.50	28.92
ASP	N	352	31.49	-44.37	27.39	:	ASP	CA	352	32.32	32.32	26.84
ASP	CB	352	33.29	-43.89	25.84	:	ASP	CG	352	34.44	34.44	26.56
ASP	OD1	352	34.15	-45.34	27.51	:	ASP	OD2	352	35.61	35.61	26.18
ASP	C	352	31.52	-42.20	26.17	:	ASP	O	352	31.62	31.62	26.47
VAL	N	353	30.54	-42.70	25.39	:	VAL	CA	353	29.67	29.67	24.57
VAL	CB	353	28.67	-42.68	23.76	:	VAL	CG1	353	27.96	27.96	22.80
VAL	CG2	353	29.40	-43.77	23.00	:	VAL	C	353	28.92	28.92	25.56
VAL	O	353	28.97	-39.78	25.44	:	LEU	N	354	28.33	28.33	26.60
LEU	CA	354	27.64	-40.81	27.61	:	LEU	CB	354	27.01	27.01	28.63
LEU	CG	354	25.69	-42.35	28.30	:	LEU	CD1	354	25.00	25.00	29.54
LEU	CD2	354	24.73	-41.28	27.84	:	LEU	C	354	28.63	28.63	28.28
LEU	O	354	28.32	-38.72	28.50	:	GLY	N	355	29.86	29.86	28.49
GLY	CA	355	30.84	-39.42	29.12	:	GLY	C	355	31.21	31.21	28.34
GLY	O	355	31.45	-37.10	28.99	:	LEU	N	356	31.23	31.23	26.98
LEU	CA	356	31.55	-37.08	26.16	:	LEU	CB	356	32.10	32.10	24.83

FIG. 1.24.

LEU	CG	356	33.37	-38.20	24.78	:	LEU	CD1	356	33.32	33.32	23.64
LEU	CD2	356	34.49	-37.20	24.74	:	LEU	C	356	30.27	30.27	25.89
LEU	O	356	30.27	-35.10	25.58	:	THR	N	357	29.12	29.12	26.01
THR	CA	357	27.83	-36.31	25.86	:	THR	CB	357	26.70	26.70	25.68
THR	OG1	357	26.92	-38.07	24.49	:	THR	CG2	357	25.35	25.35	25.58
THR	C	357	27.53	-35.47	27.09	:	THR	O	357	26.79	26.79	26.87
PHE	N	358	28.02	-35.62	28.33	:	PHE	CA	358	27.39	27.39	29.47
PHE	CB	358	26.47	-35.97	30.09	:	PHE	CG	358	25.06	25.06	29.59
PHE	CD1	358	24.36	-34.84	29.44	:	PHE	CD2	358	24.47	24.47	29.34
PHE	CE1	358	23.04	-34.89	29.05	:	PHE	CE2	358	23.16	23.16	28.94
PHE	CZ	358	22.44	-36.11	28.80	:	PHE	C	358	28.24	28.24	30.59
PHE	O	358	27.73	-34.15	31.70	:	SER	N	359	29.52	29.52	30.46
SER	CA	359	30.38	-33.45	31.53	:	SER	CB	359	29.74	29.74	32.60
SER	OG	359	28.66	-31.61	32.20	:	SER	C	359	30.75	30.75	32.29
SER	O	359	31.70	-35.39	31.86	:	GLY	N	360	29.89	29.89	33.24
GLY	CA	360	30.18	-36.17	34.16	:	GLY	C	360	30.62	30.62	33.47
GLY	O	360	30.41	-37.67	32.29	:	SER	N	361	31.29	31.29	34.22
SER	CA	361	31.74	-39.47	33.66	:	SER	CB	361	32.51	32.51	34.78
SER	OG	361	31.66	-40.19	35.95	:	SER	C	361	30.59	30.59	33.15
SER	O	361	29.51	-40.44	33.77	:	GLY	N	362	30.79	30.79	32.08
GLY	CA	362	29.83	-42.22	31.71	:	GLY	C	362	29.30	29.30	32.90
GLY	O	362	28.19	-43.64	32.91	:	ASP	N	363	30.08	30.08	33.97
ASP	CA	363	29.68	-43.82	35.15	:	ASP	CB	363	30.94	30.94	35.85
ASP	CG	363	30.95	-45.76	35.56	:	ASP	OD1	363	31.71	31.71	34.69
ASP	OD2	363	30.09	-46.47	36.16	:	ASP	C	363	28.80	28.80	36.09
ASP	O	363	27.92	-43.68	36.73	:	GLU	N	364	29.17	29.17	36.27
GLU	CA	364	28.36	-40.89	37.06	:	GLU	CB	364	29.01	29.01	37.10
GLU	CG	364	29.84	-39.47	38.34	:	GLU	CD	364	30.59	30.59	38.50
GLU	OE1	364	30.40	-37.53	39.55	:	GLU	OE2	364	31.36	31.36	37.61
GLU	C	364	26.95	-40.73	36.45	:	GLU	O	364	25.93	25.93	37.14
VAL	N	365	26.86	-40.40	35.14	:	VAL	CA	365	25.58	25.58	34.51
VAL	CB	365	25.75	-39.58	33.07	:	VAL	CG1	365	26.75	26.75	32.21
VAL	CG2	365	24.43	-39.73	32.35	:	VAL	C	365	24.90	24.90	34.47
VAL	O	365	23.70	-41.51	34.75	:	MET	N	366	25.51	25.51	34.27
MET	CA	366	24.71	-43.98	34.29	:	MET	CB	366	25.50	25.50	34.01
MET	CG	366	25.73	-45.78	32.58	:	MET	SD	366	24.18	24.18	31.65
MET	CE	366	23.34	-47.27	32.56	:	MET	C	366	24.05	24.05	35.66
MET	O	366	22.87	-44.55	35.78	:	LYS	N	367	24.80	24.80	36.71
LYS	CA	367	24.41	-44.04	38.09	:	LYS	CB	367	25.51	25.51	39.03
LYS	CG	367	26.21	-44.63	39.88	:	LYS	CD	367	27.21	27.21	39.04
LYS	CE	367	28.63	-45.39	39.71	:	LYS	NZ	367	29.74	29.74	38.73
LYS	C	367	23.15	-43.27	38.42	:	LYS	O	367	22.15	22.15	38.91
LEU	N	368	23.23	-41.99	38.09	:	LEU	CA	368	22.13	22.13	38.34
LEU	CB	368	22.56	-39.70	37.96	:	LEU	CG	368	21.53	21.53	37.67
LEU	CD1	368	21.08	-37.93	38.94	:	LEU	CD2	368	22.17	22.17	36.66
LEU	C	368	20.93	-41.47	37.50	:	LEU	O	368	19.80	19.80	38.01
ILE	N	369	21.17	-42.00	36.29	:	ILE	CA	369	20.06	20.06	35.42
ILE	CB	369	20.67	-42.72	34.00	:	ILE	CG2	369	19.88	19.88	33.20
ILE	CG1	369	20.72	-41.40	33.22	:	ILE	CD1	369	19.35	19.35	32.98
ILE	C	369	19.38	-43.54	36.14	:	ILE	O	369	18.16	18.16	36.31
ASN	N	370	20.22	-44.40	36.69	:	ASN	CA	370	19.67	19.67	37.50
ASN	CB	370	20.75	-46.52	37.64	:	ASN	CG	370	20.60	20.60	36.39
ASN	OD1	370	21.46	-47.53	35.50	:	ASN	ND2	370	19.41	19.41	36.22
ASN	C	370	19.07	-45.03	38.86	:	ASN	O	370	18.37	18.37	39.40
LYS	N	371	19.21	-43.82	39.43	:	LYS	CA	371	18.56	18.56	40.72
LYS	CB	371	18.79	-42.03	41.22	:	LYS	CG	371	20.26	20.26	41.48
LYS	CD	371	20.31	-40.52	42.58	:	LYS	CE	371	21.71	21.71	42.92
LYS	NZ	371	22.07	-38.78	42.07	:	LYS	C	371	17.04	17.04	40.81
LYS	O	371	16.53	-43.99	41.88	:	GLN	N	372	16.31	16.31	39.70

FIG. 1.25.

GLN	CA	372	14.85	-43.40	39.69	:	GLN	CB	372	14.36	14.36	38.33
GLN	CG	372	12.85	-42.91	38.06	:	GLN	CD	372	11.94	11.94	39.08
GLN	OE1	372	11.26	-43.03	39.74	:	GLN	NE2	372	11.83	11.83	39.23
GLN	C	372	14.09	-44.64	40.08	:	GLN	O	372	13.65	13.65	41.23
SER	N	373	13.81	-45.64	39.24	:	SER	CA	373	13.16	13.16	39.59
SER	CB	373	13.05	-47.30	41.11	:	SER	OG	373	12.07	12.07	41.85
SER	C	373	11.75	-46.91	39.10	:	SER	O	373	11.28	11.28	38.67
GLY	N	374	11.14	-45.73	39.18	:	GLY	CA	374	9.82	9.82	38.63
GLY	C	374	9.85	-45.66	37.11	:	GLY	O	374	10.92	10.92	36.48
SER	N	375	8.69	-45.82	36.53	:	SER	CA	375	8.63	8.63	35.10
SER	CB	375	8.60	-47.31	34.67	:	SER	OG	375	9.83	9.83	34.93
SER	C	375	7.40	-45.13	34.60	:	SER	O	375	6.30	6.30	35.11
TYR	N	376	7.59	-44.29	33.60	:	TYR	CA	376	6.57	6.57	32.95
TYR	CB	376	5.47	-44.40	32.40	:	TYR	CG	376	5.78	5.78	31.00
TYR	CD1	376	6.82	-45.79	30.73	:	TYR	CE1	376	7.09	7.09	29.46
TYR	CD2	376	4.97	-44.53	29.98	:	TYR	CE2	376	5.21	5.21	28.69
TYR	CZ	376	6.27	-45.78	28.45	:	TYR	OH	376	6.51	6.51	27.15
TYR	C	376	5.99	-42.49	33.92	:	TYR	O	376	6.48	6.48	33.94
PHE	N	377	5.01	-42.81	34.74	:	PHE	CA	377	4.44	4.44	35.61
PHE	CB	377	2.97	-42.10	35.76	:	PHE	CG	377	2.31	2.31	34.41
PHE	CD1	377	2.13	-43.48	33.89	:	PHE	CD2	377	1.91	1.91	33.71
PHE	CE1	377	1.54	-43.62	32.67	:	PHE	CE2	377	1.34	1.34	32.49
PHE	CZ	377	1.15	-42.51	31.97	:	PHE	C	377	5.21	5.21	36.91
PHE	O	377	5.66	-42.97	37.33	:	VAL	N	378	5.41	5.41	37.57
VAL	CA	378	6.26	-40.66	38.74	:	VAL	CB	378	7.61	7.61	38.10
VAL	CG1	378	8.25	-39.09	38.78	:	VAL	CG2	378	8.55	8.55	38.18
VAL	C	378	5.65	-39.65	39.73	:	VAL	O	378	4.96	4.96	39.34
ASP	N	379	5.91	-39.84	41.01	:	ASP	CA	379	5.44	5.44	42.06
ASP	CB	379	5.80	-39.55	43.36	:	ASP	CG	379	5.13	5.13	44.54
ASP	OD1	379	5.57	-39.19	45.67	:	ASP	OD2	379	4.18	4.18	44.35
ASP	C	379	6.17	-37.63	41.94	:	ASP	O	379	7.41	7.41	41.87
ALA	N	380	5.55	-36.42	41.94	:	ALA	CA	380	6.34	6.34	41.62
ALA	CB	380	6.54	-35.06	40.13	:	ALA	C	380	5.94	5.94	42.07
ALA	OT1	380	4.96	-33.32	41.55	:	ALA	OT2	380	6.68	6.68	42.84

FIG. 2a.

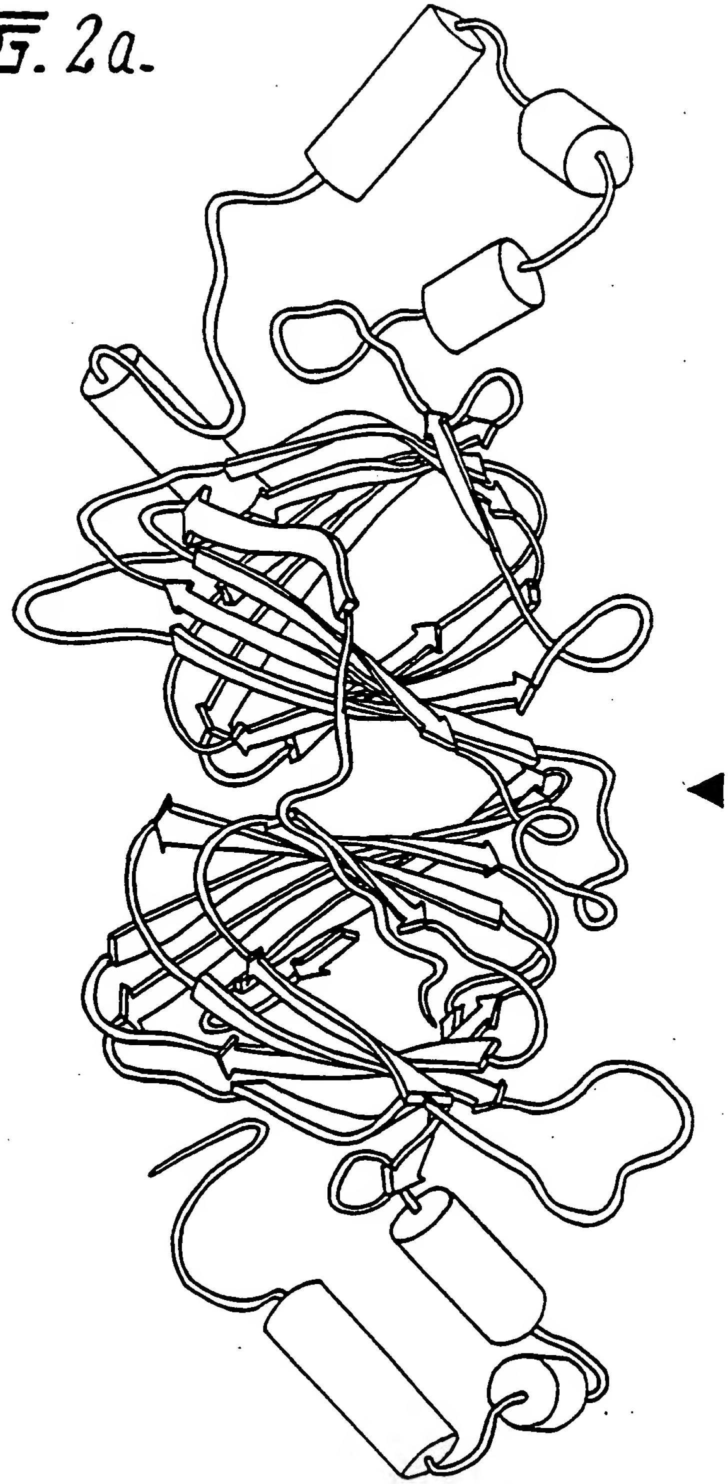


FIG. 2b.

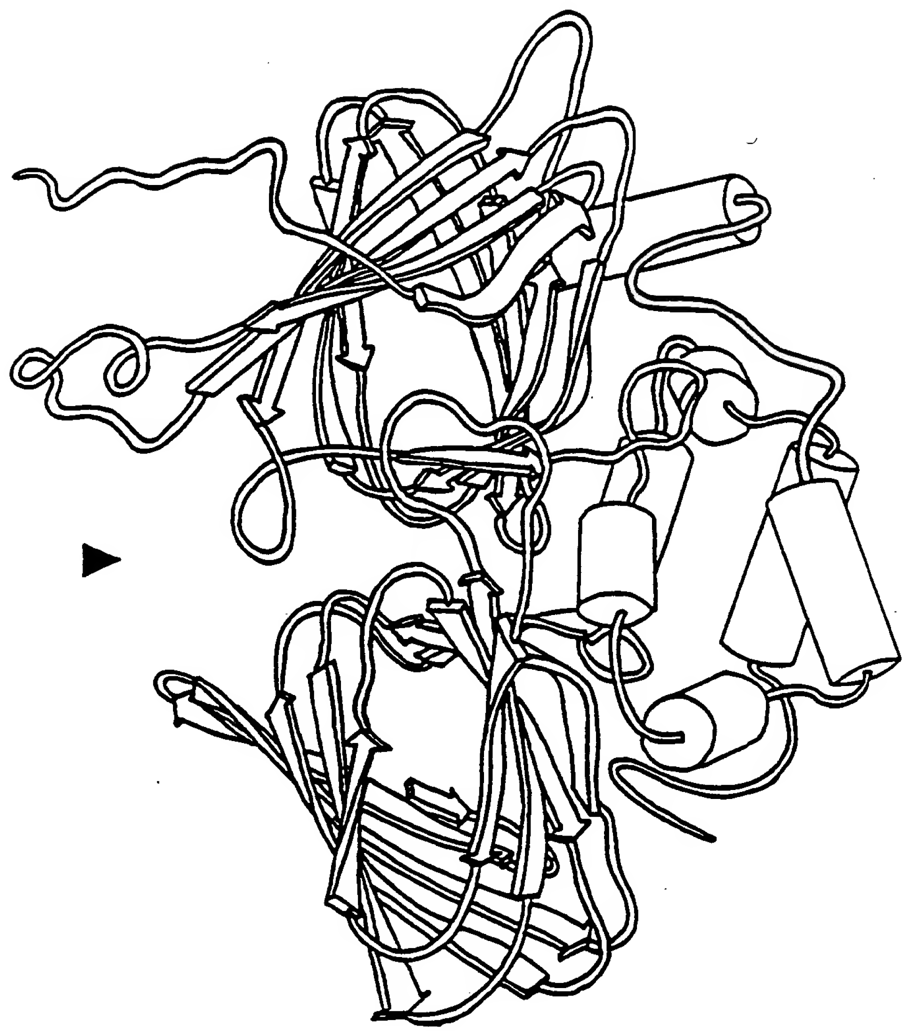
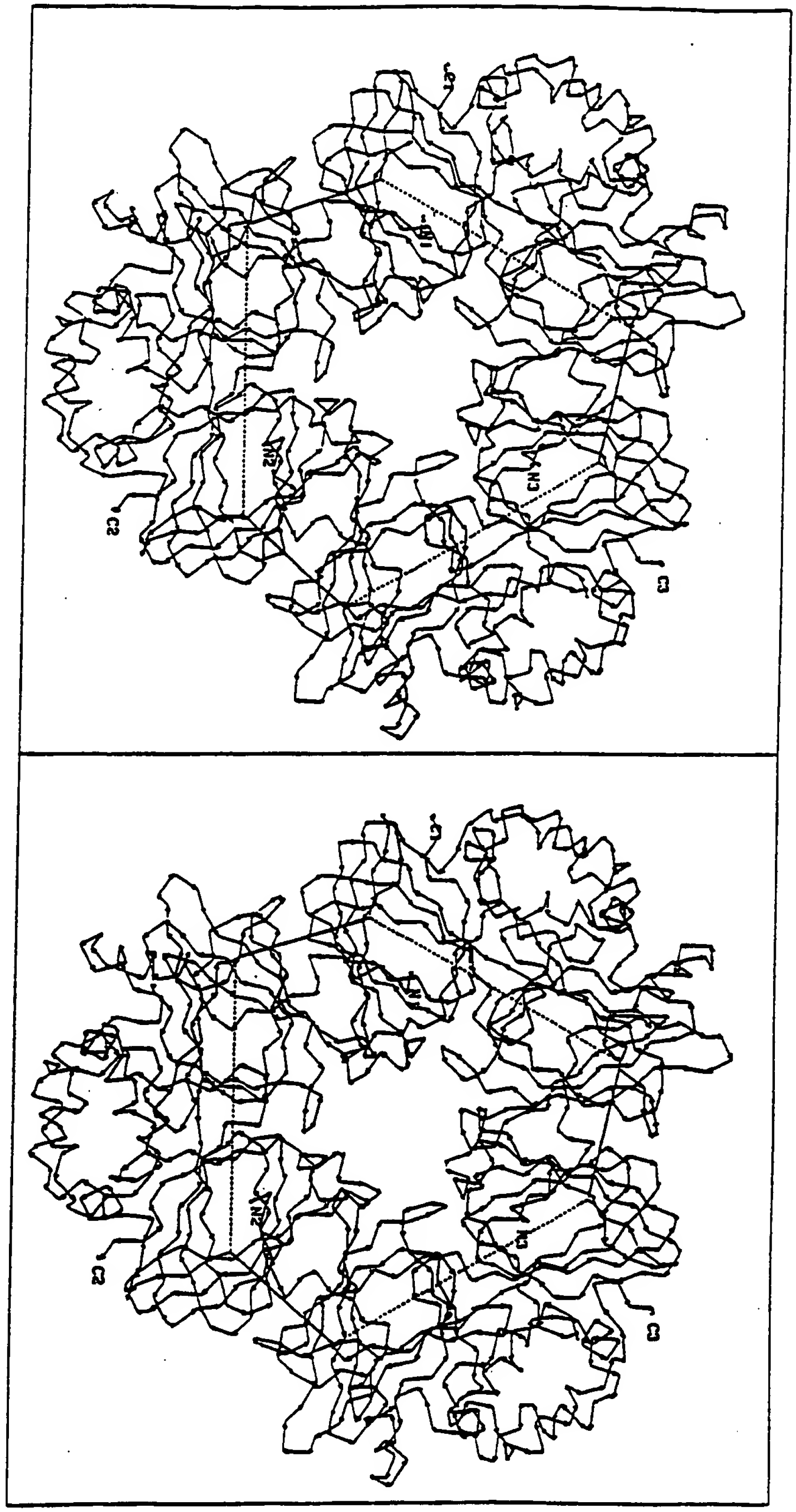
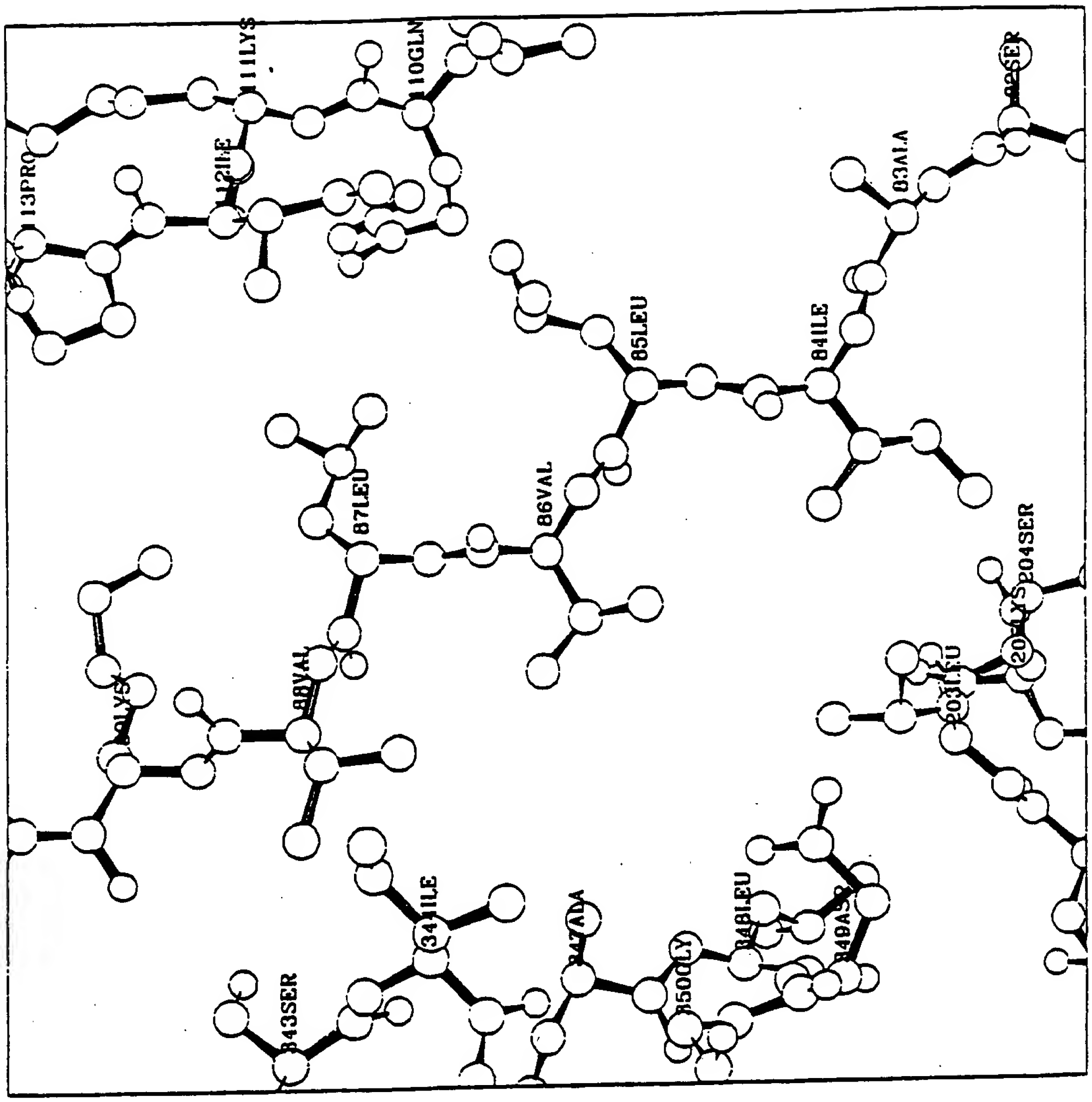


FIG. 3.




113PRO
111LYS
110GLN
83ALA
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84ILE
86VAL
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204SER
88VAL
343SER
344ILE
348LEU
350GLY

FIG. 4A.

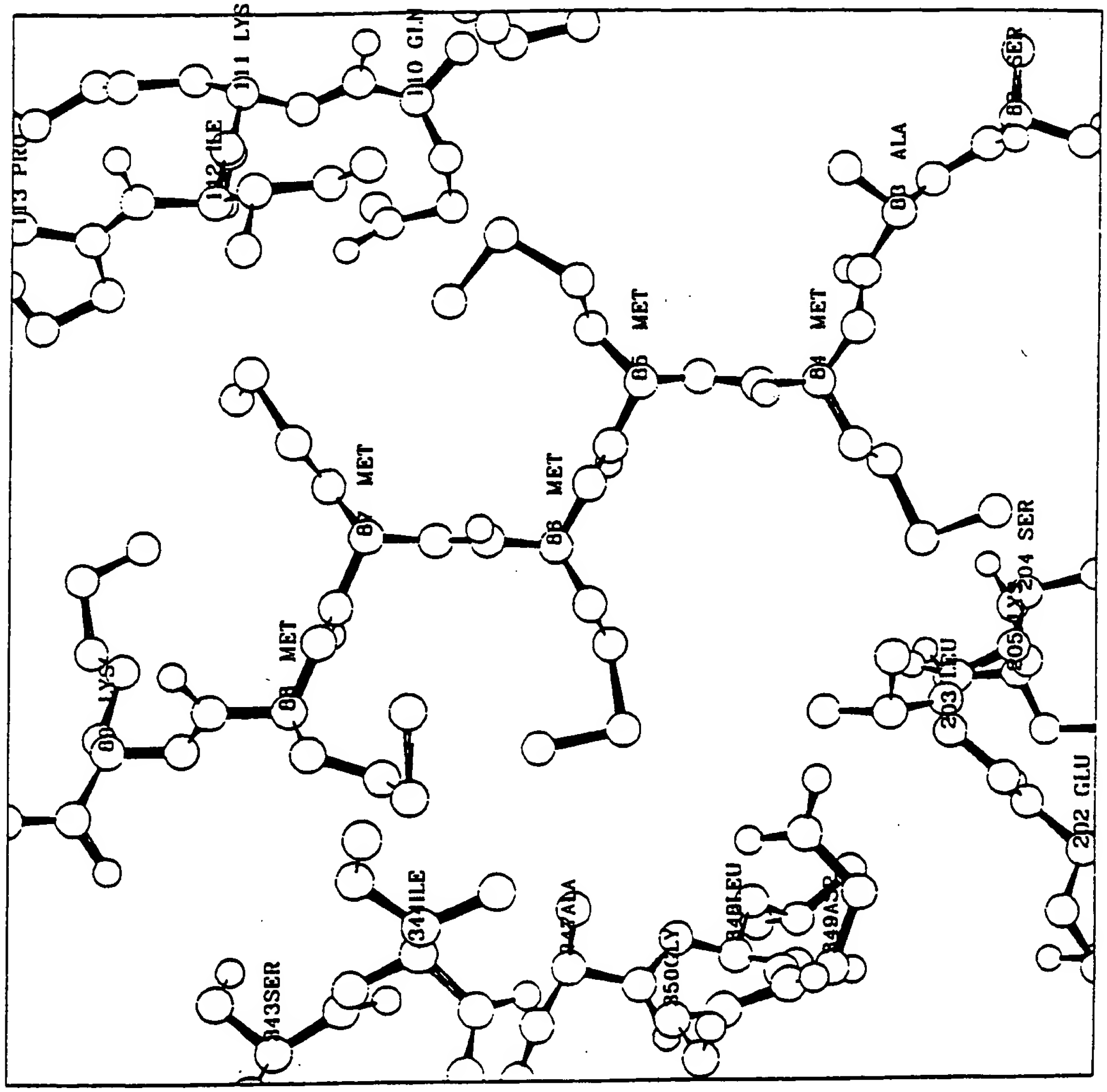

FIG. 4B.

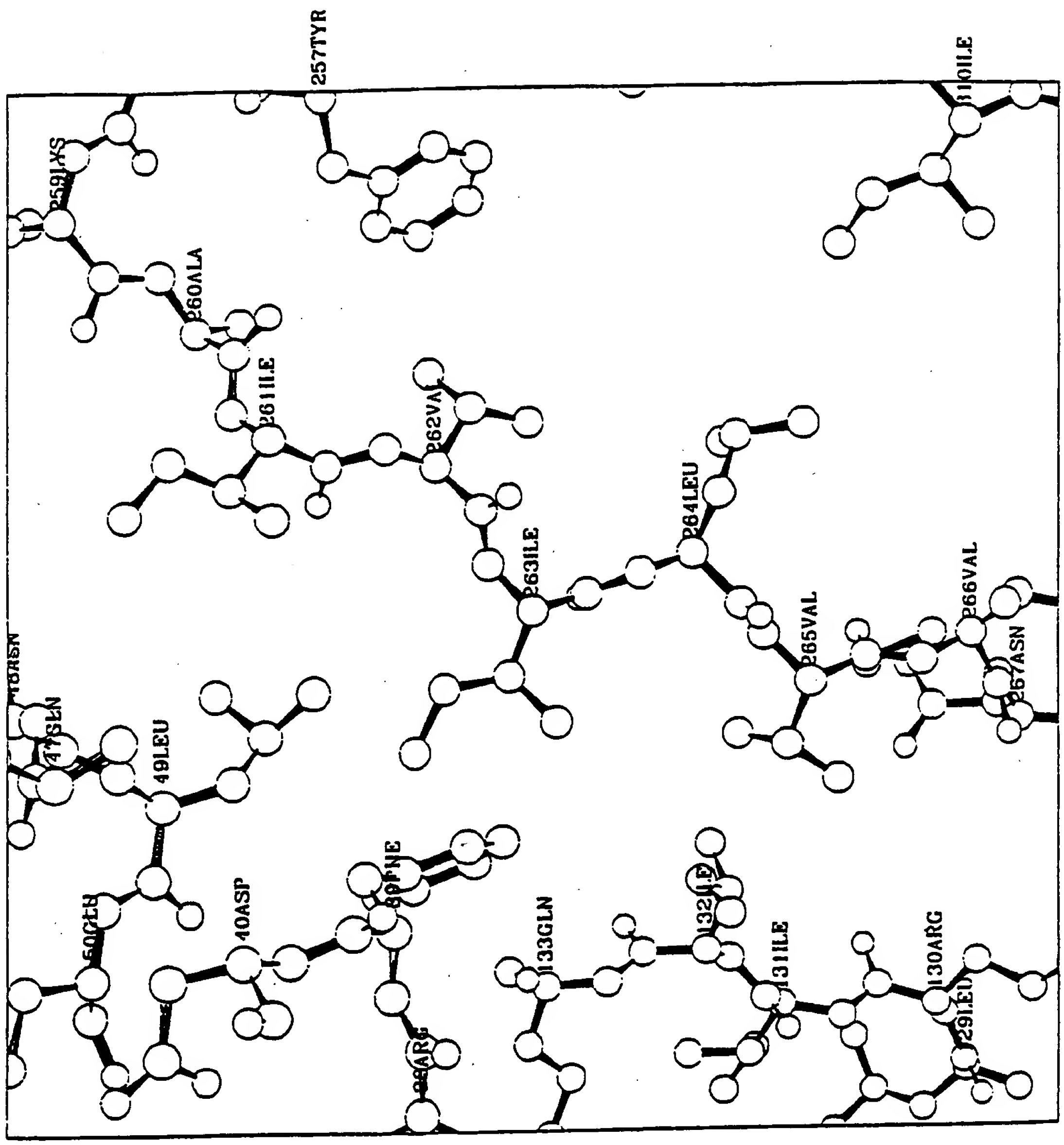
257TYR
259LYS
260ALA
261ILE
262VAL
263ILE
264LEU
265VAL
266VAL
267ASN
47GLN
49LEU
40ASP
133GLN
131ILE
130ARG

FIG. 5A.

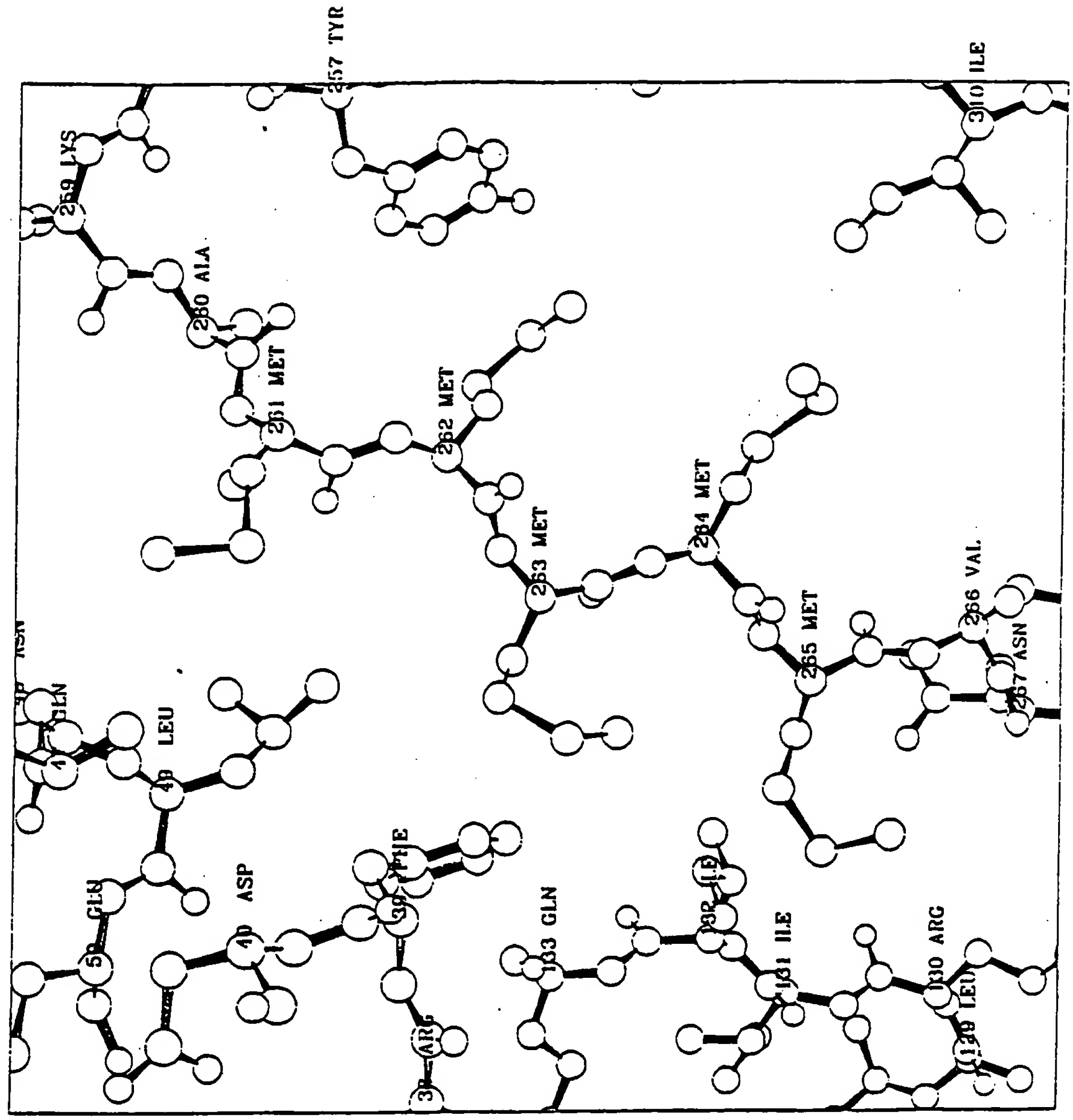
257 TYR
310 ILE
259 LYS
260 ALA
261 MET
262 MET
263 MET
264 MET
265 MET
266 VAL
267 ASN
GLN
LEU
ASP
GLN
133 GLN
131 ILE
130 ARG
ARG

FIG. 5B.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/AU 90/00430

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) 6

According to International Patent Classification (IPC) or to both National Classification and IPC

Int. Cl.5 C07K 13/00, C12N 15/29, A01H 5/00, A01H 5/10, 1/00, C12N 1/21 // (C12N 1/21, C12R 1:01)

II. FIELDS SEARCHED

Minimum Documentation Searched 7

Classification System	Classification Symbols
IPC	WPAT, USPM DERWENT DATABASE KEYWORDS: SEED STORAGE PROTEIN

Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched 8

AU: C12N 15/29, C07K 13/00; CHEMICAL ABSTRACTS KEYWORDS AS ABOVE AND BIOTECHNOLOGY DERWENT DATABASE KEYWORDS AS ABOVE, ADDITIONAL KEYWORDS: MUTEIN, MUTANT, VARIANT, MODIFIED, MODIFICATION

III. DOCUMENTS CONSIDERED TO BE RELEVANT 9

Category*	Citation of Document, 11 with indication, where appropriate, of the relevant passages 12	Relevant to Claim No 13
P,A	Protein Engineering, volume 3, no. 8, 1990, pp. 725-731, Chan-Shick Kim <u>et al</u>., "Improvement of nutritional value and functional properties of soybean glycinin by protein engineering, "whole document.	(1-13)
A	Plant Molecular Biology, vol 11, 1988, pp. 717-729, L.M. Hoffman <u>et al</u>., "A modified storage protein is synthesized, processed, and degraded in the seeds of transgenic plants", whole document.	(1-16)
A	Biochem. Physiol. Pflanzen, 183, 1988 pp. 211-218, Gerhard Saalbach <u>et al</u>., "Construction of storage protein genes with increased number of methionine codons and their use in transformation experiments", whole document.	(1-16)

(continued)

* Special categories of cited documents: 10

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed
- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
3 January 1991 (03.01.91)	10 January 1991
International Searching Authority	**Signature of Authorized Officer**
Australian Patent Office	M.E. KEESE

FURTHER INFORMATION CONTINUED FROM THE SECOND SHEET

A	Nature, volume 339, 29 June 1989, pp. 658-659, Dagmar Ringe, "The sheep in wolf's clothing", whole document.	(1-13)
A	Fed. Proc. Fed. Am. Soc. Exptl. Biol; vol 46, 6, p. 2023 C.D. Dickinson et al., "Engineering of soybean seed storage proteins", abstract.	(1-13)

V. [] OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE 1

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.[] Claim numbers ..., because they relate to subject matter not required to be searched by this Authority, namely:

2.[] Claim numbers ..., because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3.[] Claim numbers ..., because they are dependent claims and are not drafted in accordance with the second and third sentences of PCT Rule 6.4 (a):

VI. [] OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING 2

This International Searching Authority found multiple inventions in this international application as follows:

1. [] As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims of the international application.
2. [] As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims of the international application for which fees were paid, specifically claims:
3. [] No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:
4. [] As all searchable claims could be searched without effort justifying an additional fee, the International Searching Authority did not invite payment of any additional fee.

Remark on Protest

[] The additional search fees were accompanied by applicant's protest.

[] No protest accompanied the payment of additional search fees.